

BLAST Basic Local Alignment Search ToolJob Title: M18930:Human hepsin mRNA, complete cds

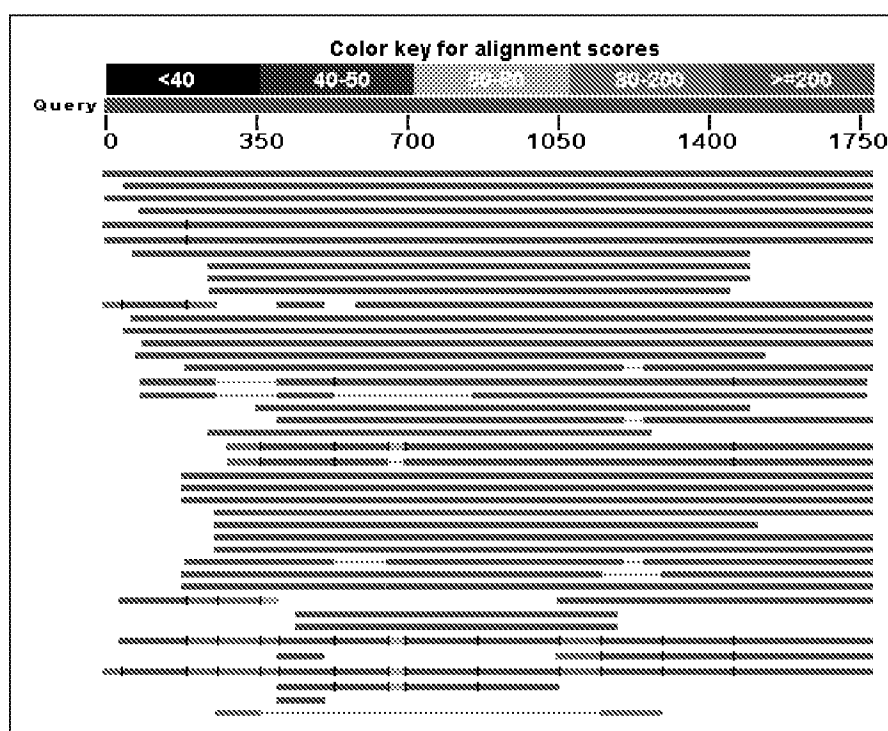
•
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BLASTN 2.2.18+

RID: 36C7FNM2013 **Database:** All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences) 6,839,787 sequences; 23,768,953,950 total letters

Query= gi|184371|gb|M18930.1|HUMHPSNA Human hepsin mRNA, complete cds. Length=1783

Distribution of 106 Blast Hits on the Query Sequence



[Distance tree of results](#)


Legend for links to other resources: UniGene GEO Gene Structure Map Viewer

Sequences producing significant alignments:
 (Click headers to sort columns)

NM_002151.1	Homo sapiens hepsin (transmembrane protease, serine 1) (HPN), transcript variant 2, mRNA >gb M18930.1 HUMHPSNA Human hepsin mRNA, complete cds	3293	3293	100%	0.0	100%	
BC025716.1	Homo sapiens hepsin (transmembrane protease, serine 1), mRNA (cDNA clone MGC:34588 IMAGE:5228525), complete cds	3199	3199	97%	0.0	99%	
XM_001093578.1	PREDICTED: Macaca mulatta hepsin (transmembrane protease, serine 1), transcript variant 2 (HPN), mRNA	3057	3057	99%	0.0	97%	
CR860913.1	Pongo abelii mRNA; cDNA DKFZp469A1831 (from clone DKFZp469A1831)	3000	3000	95%	0.0	98%	
NM_182983.1	Homo sapiens hepsin (transmembrane protease, serine 1) (HPN), transcript variant 1, mRNA >emb X07732.1 HSHEPSH Human hepatoma mRNA for serine protease hepsin	2942	3300	100%	0.0	100%	
XM_001093699.1	PREDICTED: Macaca mulatta hepsin (transmembrane protease, serine 1), transcript variant 3 (HPN), mRNA	2754	3063	99%	0.0	97%	
AK315655.1	Homo sapiens cDNA, FLJ96746	2645	2645	80%	0.0	100%	
DQ895314.2	Synthetic construct Homo sapiens clone IMAGE:100009774; FLH183201.01L; RZPD0839H04139D hepsin (transmembrane protease, serine 1) (HPN) gene, encodes complete protein	2309	2309	70%	0.0	99%	
DQ892119.2	Synthetic construct clone IMAGE:100004749; FLH183205.01X; RZPD0839H04140D hepsin (transmembrane protease, serine 1) (HPN) gene, encodes complete protein	2309	2309	70%	0.0	99%	
EU644753.1	Homo sapiens truncated hepsin serine protease mRNA, complete cds	2228	2228	67%	0.0	100%	
X07002.1	H.sapiens liver mRNA for serine protease hepsin	2215	2215	67%	0.0	100%	
AK233353.1	Sus scrofa mRNA, clone:LVRM10127D02, expressed in liver	2069	2069	96%	0.0	88%	
NM_001080241.2	Bos taurus hepsin (transmembrane protease, serine 1) (HPN), mRNA >gb BC140636.1 Bos taurus hepsin (transmembrane protease, serine 1), mRNA (cDNA clone MGC:148484 IMAGE:8196479), complete cds	1973	1973	97%	0.0	87%	
BT029913.1	Bos taurus hepsin (transmembrane protease, serine 1) (HPN), mRNA, complete cds	1956	1956	94%	0.0	87%	
XM_541697.2	PREDICTED: Canis familiaris similar to Serine protease hepsin (Transmembrane protease, serine 1) (LOC484583), mRNA	1873	1873	81%	0.0	89%	
XM_001157575.1	PREDICTED: Pan troglodytes hepsin (transmembrane protease, serine 1), transcript variant 2 (HPN), mRNA	1868	2836	86%	0.0	99%	
CR597177.1	full-length cDNA clone CS0DJ003YL08 of T cells (Jurkat cell 1714 line) Cot 10-normalized of Homo sapiens (human)	2852	2852	86%	0.0	100%	
CR592189.1	full-length cDNA clone CS0DM012Y015 of Fetal liver of Homo sapiens (human)	1663	2235	68%	0.0	100%	
CU693029.1	Synthetic construct Homo sapiens gateway clone IMAGE:100019300 3' read HPN mRNA	1653	1653	64%	0.0	92%	
XM_001157514.1	PREDICTED: Pan troglodytes hepsin (transmembrane protease, serine 1), transcript variant 1 (HPN), mRNA	1476	2445	74%	0.0	99%	
CU693028.1	Synthetic construct Homo sapiens gateway clone IMAGE:100019300 5' read HPN mRNA	1465	1465	57%	0.0	92%	
AK095160.1	Homo sapiens cDNA FLJ37841 fis, clone BRSSN2012081, highly similar to SERINE PROTEASE HEPsin (EC 3.4.21.-)	1404	2782	83%	0.0	100%	
XM_001093460.1	PREDICTED: Macaca mulatta hepsin (transmembrane protease, serine 1), transcript variant 1 (HPN), mRNA	1360	2552	81%	0.0	98%	
NM_008281.3	Mus musculus hepsin (Hpn), transcript variant 2, mRNA	1303	1303	89%	0.0	81%	
NM_017112.1	Rattus norvegicus hepsin (Hpn), mRNA >emb X70900.1 RNHEPA R.norvegicus mRNA for hepsin	1297	1297	89%	0.0	81%	
AF030065.1	Mus musculus serine protease hepsin mRNA, complete cds	1280	1280	89%	0.0	81%	
NM_001110252.1	Mus musculus hepsin (Hpn), transcript variant 1, mRNA	1245	1245	85%	0.0	81%	
BC138809.1	Mus musculus hepsin, mRNA (cDNA clone MGC:170436 IMAGE:8861831), complete cds	1240	1240	70%	0.0	84%	
AK156553.1	Mus musculus activated spleen cDNA, RIKEN full-length enriched library, clone:F830029I12 product:hepsin, full insert sequence	1240	1240	85%	0.0	81%	
AK002694.1	Mus musculus adult male kidney cDNA, RIKEN full-length	1181	1181	85%	0.0	81%	

	enriched library, clone:0610030A17 product:hepsin, full insert sequence							
XM_512584.2	PREDICTED: Pan troglodytes hepsin (transmembrane protease, serine 1), transcript variant 3 (HPN), mRNA	1011	2618	79%	0.0	100%		
BC072688.1	Rattus norvegicus hepsin, mRNA (cDNA clone MGC:91742 IMAGE:7098661), complete cds	935	1200	82%	0.0	84%		
AY234104.1	Mus musculus truncated hepsin splice variant mRNA, complete cds; alternatively spliced	880	1283	89%	0.0	82%		
XM_001254640.1	PREDICTED: Bos taurus similar to hepsin (LOC787164), partial mRNA	815	815	41%	0.0	86%		
BC119448.1	Mus musculus cDNA clone IMAGE:40044314	717	717	41%	0.0	84%		
BC119449.1	Mus musculus cDNA clone IMAGE:40044315	712	712	41%	0.0	84%		
AC192150.4	Pan troglodytes BAC clone CH251-522E19 from chromosome 19, complete sequence	590	3279	97%	9e-165	100%		
AK091988.1	Homo sapiens cDNA FLJ34669 fis, clone LIVER2001051	590	1367	41%	9e-165	100%		
AC020907.6	Homo sapiens chromosome 19 clone CTD-2527I21, complete sequence	590	3376	100%	9e-165	100%		
AK125670.1	Homo sapiens cDNA FLJ43682 fis, clone TBAES2001258, weakly similar to SERINE PROTEASE HEPSIN (EC 3.4.21.-)	353	1228	36%	1e-93	100%		
DQ677665.1	Homo sapiens sodium channel beta-1 subunit precursor (SCN1B) gene, complete cds	289	509	14%	4e-74	100%		
AC197610.3	MACACA MULATTA BAC clone CH250-348G8 from chromosome 19, complete sequence	250	637	20%	2e-62	98%		
XM_001719305.1	PREDICTED: Homo sapiens hypothetical protein LOC100128675 (LOC100128675), mRNA	207	207	6%	1e-49	100%		
XM_001721961.1	PREDICTED: Homo sapiens hypothetical protein LOC100128675 (LOC100128675), mRNA	207	207	6%	1e-49	100%		
XM_001719287.1	PREDICTED: Homo sapiens hypothetical protein LOC100128675 (LOC100128675), mRNA	207	207	6%	1e-49	100%		
AC158993.2	Mus musculus BAC clone RP24-427N13 from chromosome 7, complete sequence	141	260	13%	1e-29	87%		

Alignments

>ref|NM_002151.1|  Homo sapiens hepsin (transmembrane protease, serine 1) (HPN), transcript variant 2, mRNA

gb|M18930.1|HUMHPSNA  Human hepsin mRNA, complete cds
Length=1783

GENE ID: 3249 HPN | hepsin (transmembrane protease, serine 1) [Homo sapiens]
(Over 10 PubMed links)


Score = 3293 bits (1783), Expect = 0.0
Identities = 1783/1783 (100%), Gaps = 0/1783 (0%)
Strand=Plus/Plus

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>gb|BC025716.1|  Homo sapiens hepsin (transmembrane protease, serine 1), mRNA
(cDNA clone MGC:34588 IMAGE:5228525), complete cds
Length=1761

GENE ID: 3249 HPN | hepsin (transmembrane protease, serine 1) [Homo sapiens]
(Over 10 PubMed links)

Score = 3199 bits (1732), Expect = 0.0
Identities = 1734/1735 (99%), Gaps = 0/1735 (0%)
Strand=Plus/Plus

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>ref|XM_001093578.1|  PREDICTED: Macaca mulatta hepsin (transmembrane protease, serine 1), transcript variant 2 (HPN), mRNA
Length=1785

GENE ID: 707242 HPN | hepsin (transmembrane protease, serine 1)
[Macaca mulatta]

Score = 3057 bits (1655), Expect = 0.0
Identities = 1739/1781 (97%), Gaps = 0/1781 (0%)
Strand=Plus/Plus

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Query 543 ACCCACTCCGAGCTGGACGTGCGAACGGCGGGCGCCAATGGCACGTGCGGGCTTCTTCTGT 602
Sbjct 543 ACCCACTCCGAGTTGGACGTGCGAACGGCGGGCGCCAACGGCACGTGAGGCTTCTTCTGT 602

Query 603 GTGGACGAGGGGAGGCTGCCCCACACCCAGAGGCTGCTGGAGGTGATCTCCGTGTGTGAT 662
Sbjct 603 GTGGATGAGGGGAGGCTGCCACACACCCAGAGGCTGCTGGAGGTGATCTCCGTGTGTGAC 662

Query 663 TGCCCCAGAGGCCGTTTCTTGCCCGCCATCTGCCAAGACTGTGGCCGAGGAAGCTGCCC 722
Sbjct 663 TGTCCCAGAGGCCGTTTCTTGCCCACCGTCTGCCAAGACTGTGGCCGAGGAAGCTGCCC 722

Query 723 GTGGACCGCATCGTGGGAGGCCGGGACACCAGCTTGGGCCGCTGGCCGTGGCAAGTCAGC 782
Sbjct 723 GTGGACCGCATCGTGGGAGGCCGGGACACCAGCTTGGGCCGCTGGCCGTGGCAAGTCAGC 782

Query 783 CTTGCTATGATGGAGCACACCTCTGTGGGGGATCCCTGCTCTCCGGGGACTGGGTGCTG 842
Sbjct 783 CTTGCTATGATGGAGCACACCTCTGCGGGGGGTCCCTGCTCTCCGGGGACTGGGTGCTG 842

Query 843 ACAGCCGCCCCACTGCTTCCCGAGCGGAACCGGGTCTGTCCCGATGGCGAGTGTTTGCC 902
Sbjct 843 ACAGCTGCCCACTGCTTCCCGAGCGGAACCGGGTCTGTCCCGATGGCGAGTGTTTGCC 902

Query 903 GGTGCCGTGGCCAGGCCTCTCCCCACGGTCTGCAGCTGGGGGTGCAGGCTGTGGTCTAC 962
Sbjct 903 GGTGCCGTGGCCAGGCCTCTCCCCACGGTCTGCAGCTGGGGGTGCAGGCTGTGGTCTAC 962

Query 963 CACGGGGGCTATCTTCCCTTTTCGGGACCCCAACAGCGAGGAGAAACAGCAACGATATTGCC 1022
Sbjct 963 CACGGGGGCTATCTTCCCTTTTCGGGACCCCAACAGCGAGGAGAAACAGCAATGATATTGCC 1022

Query 1023 CTGGTCCACCTCTCCAGTCCCCTGCCCCCTCACAGAATACATCCAGCCTGTGTGCCTCCCA 1082
Sbjct 1023 CTGGTCCACCTCTCCAGTCCCCTGCCCCCTCACAGAATACATCCAGCCTGTGTGCCTCCCA 1082

Query 1083 GCTGCCGCCAGGCCCTGGTGGATGGCAAGATCTGTACCGTGACGGGCTGGGGCAACACG 1142
Sbjct 1083 GCTGCTGCGCAGGCCCTGGTGGATGGCAAGATCTGTACCGTGACGGGCTGGGGCAACACG 1142

Query 1143 CAGTACTATGGCCAACAGGCCGGGTACTCCAGGAGGCTCGAGTCCCATAATCAGCAAT 1202
Sbjct 1143 CAGTACTATGGCCAACAGGCCGGGTACTCCAGGAGGCTCGAGTCCCATAATCAGCAAT 1202

Query 1203 GATGCTGCAATGGCGCTGACTTCTATGGAACAGATCAAGCCCAAGATGTTCTGTGCT 1262
Sbjct 1203 GATGCTGCAATGGCGCTGACTTCTATGGAACAGATCAAGCCCAAGATGTTCTGTGCT 1262

Query 1263 GGCTACCCCGAGGGTGGCATTGATGCCTGCCAGGGCGACAGCGGTGGTCCCTTTGTGTGT 1322
Sbjct 1263 GGCTACCCCGAGGGTGGCATTGATGCCTGCCAGGGTGACAGCGGTGGTCCCTTTGTGTGT 1322

Query 1323 GAGGACAGCATCTCTCGACGCCACGTTGGCGGCTGTGTGGCATTGTGAGTTGGGGCACT 1382
Sbjct 1323 GAGGACAGCATCTCTCGACGCCACGTTGGCGGCTGTGTGGCATTGTGAGTTGGGGCACT 1382

Query 1383 GGCTGTGCCCTGGCCCCAGAAGCCAGGCGTCTACACCAAAGTCAGTGACTTCCGGGAGTGG 1442
Sbjct 1383 GGCTGTGCCCTGGCCCCAGAAGCCAGGCGTCTACACCAAAGTCAGTGACTTCCGGGAGTGG 1442

Query 1443 ATCTTCCAGGCCATAAAGACTCACTCCGAAGCCAGCGGCATGGTGACCCAGCTCTGACCG 1502
Sbjct 1443 ATCTTCCAGGCCATAAAGACTCACTCCGAAGCCAGCGGCATGGTGACCCAGCTCTGACCG 1502

Query 1503 GTGGCTTCTCGCTGCGCAGCCTCCAGGGCCCGAGGTGATCCCGGTGGTGGGATCCACGCT 1562
Sbjct 1503 GTGGCTTCTCGCTGCGCAGCCTCCAGGGCCCGAGGTGATCTTGGTGGTGGGATCCACGCT 1562

Query 1563 GGGCCGAGGATGGGACGTTTTTCTTCTTGGGCCCGGTCCACAGGTCCAAGGACACCTCC 1622
Sbjct 1563 GGGCTAGGATGGGACATTTTTCTTCTTGGGCCCGGTCCACAGGTCCAAGGACACCTCC 1622

Query 1623 CTCCAGGGTCTCTCTTCCACAGTGGCGGGCCCACTCAGCCCCGAGACCAACCACTCA 1682
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Sbjct 1623      |||CCAGGGTCCTTTCTTCCACAGTGGCGGGCCCACTCAGCCCCGAGACCCCGACCTCA 1682
Query 1683      CCCTCCTGACCCCCATGTAAATATTGTTCTGCTGTCTGGGACTCCTGTCTAGGTGCCCCCT 1742
Sbjct 1683      CCCTCCTGACCCCCGTGTAAATATTGTTCTGCTGTCTGGGACTCCTGTCTAGGTGCCCCCT 1742
Query 1743      GATGATGGGATGCTCTTTAAATAATAAAGATGGTTTGTATT 1783
Sbjct 1743      GATGACGGGATGCTCTTTAAATAATAAAGATGGTTTGTATT 1783

>emb|CR860913.1| Pongo abelii mRNA; cDNA DKFZp469A1831 (from clone DKFZp469A1831)
Length=1741

Score = 3000 bits (1624), Expect = 0.0
Identities = 1676/1702 (98%), Gaps = 0/1702 (0%)
Strand=Plus/Plus



Query 82      GCCTCCAGGCCGCGCCGCTGCTGCGGGGCCACCATGCTCCTGCCAGGCCTGGAGACTGAC 141
Sbjct 18      GCCTCCAGGCCGCGCCGCTGCTGCGGGGCCACCATGCTCCTGCCAGGCCTGGAGACTGAC 77
Query 142     CCGACCCCGGCACTACCTCGAGGCTCCGCCCCACCTGCTGGACCCAGGGTCCCACCCCT 201
Sbjct 78      CCGACCCCGGCAACACCTCGAGGCTCCGCCCCACCTGCTGGACCCAGGGTCCCACCCCT 137
Query 202     GGCCCAAGGAGGTGAGCCAGGGAATCATTAAACAAGAGGCAGTGACATGGCGCAGAAGGAGG 261
Sbjct 138     GGCCCAAGGAGGTGAGCCAGGGAATCATTAAACAAGAGGCGGTGACATGGCGCAGAAGGAGG 197
Query 262     GTGGCCGGAAGTGTGCCATGCTGCTCCAGACCCAAGGTGGCAGCTCTCACTGCGGGGACCC 321
Sbjct 198     GTGGCCGGAAGTGTGCCATGCTGCTCCAGACCCAAGGTGGCAGCTCTCACTGCGGGGACCC 257
Query 322     TGCTACTTCTGACAGCCATCGGGGCGGCATCCTGGGCCATTGTGGCTGTTCTCCTCAGGA 381
Sbjct 258     TGCTACTTCTGACAGCCATCGGGGCGGCATCCTGGGCCATTGTGGCTGTTCTCCTCAGGA 317
Query 382     GTGACCAGGAGCCGCTGTACCCAGTGCAGGTCAGCTCTGCGGACGCTCGGCTCATGGTCT 441
Sbjct 318     GTGACCAGGAGCCGCTGTACCCAGTGCAGGTCAGCTCTGCGGACGCTCGGCTCATGGTCT 377
Query 442     TTGACAAGACGGAAGGGACGTGGCGGCTGTGTGCTCCTCGCGCTCCAACGCCAGGGTAG 501
Sbjct 378     TTGACAAGACGGAAGGGACGTGGCGGCTGTGTGCTCCTCGCGCTCCAACGCCAGGGTAG 437
Query 502     CCGGACTCAGCTGCGAGGAGATGGGCTTCTCAGGGCACTGACCCACTCCGAGCTGGACG 561
Sbjct 438     CCGGACTCAGCTGCGTGGAGATGGGCTTCTCAGGGCGCTGACCCACTCCGAGCTGGACG 497
Query 562     TGCGAACGGCGGGCGCCAATGGCACGTCGGGCTTCTTCTGTGTGGACGAGGGGAGGCTGC 621
Sbjct 498     TGCGAACGGCGGGCGCCAATGGCACGTCGGGCTTCTTCTGTGTGGACGAGGGGAGGCTGC 557
Query 622     CCCACACCCAGAGGCTGCTGGAGGTGATCTCCGTGTGTGATTGCCCCAGAGGCCGTTTCT 681
Sbjct 558     CCCACACCCAGAGGCTGCTGGAGGTGATCTCCGTGTGTGATTGCCCCAGAGGCCGTTTCT 617
Query 682     TGGCCGCCATCTGCCAAGACTGTGGCCGAGGAAGCTGCCCCTGGACCGCATCGTGGGAG 741
Sbjct 618     TGGCCACCATCTGCCAAGACTGTGGCCGAGGAAGCTGCCCCTGGACCGCATCGTGGGAG 677
Query 742     GCCGGGACACCAAGCTTGGGCCGGTGGCCGTGGCAAGTCAGCCTTCGCTATGATGGAGCAC 801
Sbjct 678     GCCGGGACACCAAGCTTGGGCCGGTGGCCGTGGCAAGTCAGCCTTCGCTATGATGGAGCAC 737
Query 802     ACCTCTGTGGGGGATCCCTGCTCTCCGGGACTGGGTGCTGACAGCCGCCACTGCTTCC 861
Sbjct 738     ACCTTTGTGGGGGGTCCCTGCTCTCCGGGACTGGGTGCTGACAGCCGCCACTGCTTCC 797
Query 862     CGGAGCGGAACCGGGTCTGTCCCGATGGCGAGTGTGTTGCCGGTGCCGTGGCCAGGCCT 921
Sbjct 798     CAGAGCGGAACCGGGTCTGTCCCGATGGCGAGTGTGTTGCCGGTGCCGTGGCCAGGCCT 857
Query 922     CTCCCCACGGTCTGCAGCTGGGGGTGCAGGCTGTGGTCTACCACGGGGGCTATCTTCCCT 981
Sbjct 858     CTCCCCACGGCCTGCAGCTGGCGGTGCAGGCTGTGGTCTACCATGGGGGCTATCTTCCCT 917
Query 982     TTCGGGACCCCAACAGCGAGGAGAAACAGCAACGATATTGCCCTGGTCCACCTCTCCAGTC 1041
Sbjct 918     TTCGGGACCCCAACAGCGAGGAGAAACAGCAACGATATTGCCCTGGTCCACCTCTCCAGCC 977
Query 1042    CCCTGCCCTCTCAGAGAATACATCCAGCCTGTGTGCCTCCAGCTGCCGGCCAGGCCCTGG 1101
Sbjct 978     CCCTGCCCTCTCAGAGAATACATCCAGCCTGTGTGCCTCCAGCTGCCGGCCAGGCCCTGG 1037
Query 1102    TGGATGGCAAGATCTGTACCGTGACGGGCTGGGGCAACACGCAGTACTATGGCCAAACAGG 1161
Sbjct 1038    TGGATGGCAAGATCTGTACCGTGACGGGCTGGGGCAACACGCAGTACTATGGCCAAACAGG 1097
Query 1162    CCGGGGTACTCCAGGAGGCTCGAGTCCCCATAATCAGCAATGATGTCTGCAATGGCGCTG 1221
Sbjct 1098    CCGGGGTACTCCAGGAGGCTCGAGTCCCCATAATCAGCAATGATGTCTGCAATGGCGCTG 1157
Query 1222    ACTTCTATGGAAACAGATCAAGCCCAAGATGTTCTGTGCTGGCTACCCCGAGGGTGGCA 1281
Sbjct 1158    ACTTCTATGGAAACAGATCAAGCCCAAGATGTTCTGTGCTGGCTACCCCGAGGGTGGCA 1217
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Query 1282 TTGATGCCTGCCAGGGCGACAGCGGTGGTCCCTTTGTGTGTGAGGACAGCATCTCTCGGA 1341
Sbjct 1218 TTGATGCCTGCCAGGGCGACAGCGGTGGTCCCTTTGTGTGTGAGGACAGCATCTCTCGGA 1277
Query 1342 CGCCACGTTGGCGGCTGTGTGGCATTGTGAGTTGGGGCACTGGCTGTGCCCTGGCCCAGA 1401
Sbjct 1278 CGCCACGTTGGCGGCTGTGTGGCATTGTGAGCTGGGGCACTGGCTGTGCCCTGGCCCAGA 1337
Query 1402 AGCCAGGCGTCTACACCAAAGTCAGTGACTTCCGGGAGTGGATCTTCCAGGCCATAAAGA 1461
Sbjct 1338 AGCCAGGCGTCTACACCAAAGTCAGTGACTTCCGGGAGTGGATCTTCCAGGCCATAAAGA 1397
Query 1462 CTCACCTCCGAAGCCAGCGGCATGGTGACCCAGCTCTGACCGGTGGCTTCTCGCTGCGCAG 1521
Sbjct 1398 CTCATTCCGAAGCCAGCGGCATGGTGACCCAGCTCTGACCGGTGGCTTCTCGCTGCGCAG 1457
Query 1522 CCTCCAGGGCCCCGAGGTGATCCCGGTGGTGGGATCCACGCTGGGCCGAGGATGGGACGTT 1581
Sbjct 1458 CCTCCAGGGCCCCGAGGTGATCTGGTGGTGGGATCCATGCCAGGCCTAGGATGGGACGTT 1517
Query 1582 TTTCTTCTTGGGCCCGGTCCACAGGTCCAAGGACACCCTCCCTCCAGGGTCTCTCTTCC 1641
Sbjct 1518 TTTCTTCTTGGGCCCGGTCCACAGGTCCAAGGACACCCTCCCTCCAGGGTCTCTCTTCC 1577
Query 1642 ACAGTGGCGGGCCCACTCAGCCCCGAGACCACCCAACCTCACCTCTGACCCCCATGTA 1701
Sbjct 1578 ACAGTGGCGGGCCCACTCAGCCCCGAGACCACCCAACCTCACCTCTGACCCCCATGTA 1637
Query 1702 AATATTGTTCTGCTGTCTGGGACTCCTGTCTAGGTGCCCTGATGATGGGATGCTCTTTA 1761
Sbjct 1638 AATATTGTTCTGCTGTCTGGGACTCCTGTCTAGGTGCCCTGATGACGGGATGCTCTTTA 1697
Query 1762 AATAATAAAGATGGTTTGGATT 1783
Sbjct 1698 AGTAATAAAGATGGTTTGGATT 1719

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>ref|NM_182983.1|  Homo sapiens hepsin (transmembrane protease, serine 1) (HPN), transcript variant 1, mRNA
emb|X07732.1|HSEPSH  Human hepatoma mRNA for serine protease hepsin
Length=2363

GENE ID: 3249 HPN | hepsin (transmembrane protease, serine 1) [Homo sapiens]
(Over 10 PubMed links)

Sort alignments for this subject sequence by:
E value Score Percent identity
Query start position Subject start position

Score = 2942 bits (1593), Expect = 0.0
Identities = 1593/1593 (100%), Gaps = 0/1593 (0%)
Strand=Plus/Plus

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Query 191 GGTCCCACCTTGGCCCCAGGAGGTACGCCAGGGAATCATTAACAAGAGGCAGTGACATGGC 250
Sbjct 771 GGTCCCACCTTGGCCCCAGGAGGTACGCCAGGGAATCATTAACAAGAGGCAGTGACATGGC 830
Query 251 GCAGAAGGAGGGTGGCCGGAAGTGTGCCATGCTGTCTCCAGACCCAAGGTGGCAGCTCTCAC 310
Sbjct 831 GCAGAAGGAGGGTGGCCGGAAGTGTGCCATGCTGTCTCCAGACCCAAGGTGGCAGCTCTCAC 890
Query 311 TGCGGGGACCCTGCTACTTCTGACAGCCATCGGGGCGGCATCCTGGGCCATTGTGGCTGT 370
Sbjct 891 TGCGGGGACCCTGCTACTTCTGACAGCCATCGGGGCGGCATCCTGGGCCATTGTGGCTGT 950
Query 371 TCTCCTCAGGAGTGACAGGAGCCGCTGTACCCAGTGCAGGTGAGCTCTGCGGACGCTCG 430
Sbjct 951 TCTCCTCAGGAGTGACAGGAGCCGCTGTACCCAGTGCAGGTGAGCTCTGCGGACGCTCG 1010
Query 431 GTCATGGTCTTTGACAAGACGGAAGGGACGTGGCGGCTGCTGTGCTCCTCGCGCTCCAA 490
Sbjct 1011 GTCATGGTCTTTGACAAGACGGAAGGGACGTGGCGGCTGCTGTGCTCCTCGCGCTCCAA 1070
Query 491 CGCCAGGGTAGCCGGAAGTCTGAGTGCAGGAGATGGGCTTCTCAGGGCACTGACCCACTC 550
Sbjct 1071 CGCCAGGGTAGCCGGAAGTCTGAGTGCAGGAGATGGGCTTCTCAGGGCACTGACCCACTC 1130
Query 551 CGAGCTGGAGCTGCGAACCGCGGGCGCCAATGGCACGTCGGGCTTCTTCTGTGTGGACGA 610
Sbjct 1131 CGAGCTGGAGCTGCGAACCGCGGGCGCCAATGGCACGTCGGGCTTCTTCTGTGTGGACGA 1190
Query 611 GGGGAGGCTGCCCCACACCCAGAGGTGCTGGAGGTGATCTCCGTGTGTGATTGCCCCAG 670
Sbjct 1191 GGGGAGGCTGCCCCACACCCAGAGGTGCTGGAGGTGATCTCCGTGTGTGATTGCCCCAG 1250
Query 671 AGGCCGTTTCTTGGCCGCCATCTGCCAAGACTGTGGCCGAGGAAGCTGCCCGTGGACCG 730
Sbjct 1251 AGGCCGTTTCTTGGCCGCCATCTGCCAAGACTGTGGCCGAGGAAGCTGCCCGTGGACCG 1310
Query 731 CATCGTGGGAGGCCGGGACACAGCTTGGGCCGCTGGCCGTGGCAAGTCAGCCTTCGCTA 790
Sbjct 1311 CATCGTGGGAGGCCGGGACACAGCTTGGGCCGCTGGCCGTGGCAAGTCAGCCTTCGCTA 1370
Query 791 TGATGGAGCACACCTCTGTGGGGGATCCCTGCTCTCCGGGACTGGGTGCTGACAGCCGC 850
Sbjct 1371 TGATGGAGCACACCTCTGTGGGGGATCCCTGCTCTCCGGGACTGGGTGCTGACAGCCGC 1430

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Query 851  CCACTGCTTCCCGGAGCGGAACCGGGTCCTGTCCCGATGGCGAGTGTGTCGGGTGCCGT 910
Sbjct 1431  CCACTGCTTCCCGGAGCGGAACCGGGTCCTGTCCCGATGGCGAGTGTGTCGGGTGCCGT 1490

Query 911  GGCCCAAGCCTCTCCCCACGGTCTGCAGCTGGGGGTGCAGGCTGTGGTCTACCAACGGGG 970
Sbjct 1491  GGCCCAAGCCTCTCCCCACGGTCTGCAGCTGGGGGTGCAGGCTGTGGTCTACCAACGGGG 1550

Query 971  CTATCTTCCCTTTTCGGGACCCCAACAGCGAGGAGAACAGCAACGATATTGCCCTGGTCCA 1030
Sbjct 1551  CTATCTTCCCTTTTCGGGACCCCAACAGCGAGGAGAACAGCAACGATATTGCCCTGGTCCA 1610

Query 1031  CCTCTCCAGTCCCCCTGCCCCCTCACAGAATACATCCAGCCTGTGTGCCTCCCAGCTGCCGG 1090
Sbjct 1611  CCTCTCCAGTCCCCCTGCCCCCTCACAGAATACATCCAGCCTGTGTGCCTCCCAGCTGCCGG 1670

Query 1091  CCAGGCCCTGGTGGATGGCAAGATCTGTACCGTGACGGGCTGGGGCAACACGCAGTACTA 1150
Sbjct 1671  CCAGGCCCTGGTGGATGGCAAGATCTGTACCGTGACGGGCTGGGGCAACACGCAGTACTA 1730

Query 1151  TGGCCAACAGGCCGGGGTACTCCAGGAGGCTCGAGTCCCCATAATCAGCAATGATGTCTG 1210
Sbjct 1731  TGGCCAACAGGCCGGGGTACTCCAGGAGGCTCGAGTCCCCATAATCAGCAATGATGTCTG 1790

Query 1211  CAATGGCGCTGACTTCTATGAAACAGATCAAGCCCAGATGTTCTGTGCTGGCTACCC 1270
Sbjct 1791  CAATGGCGCTGACTTCTATGAAACAGATCAAGCCCAGATGTTCTGTGCTGGCTACCC 1850

Query 1271  CGAGGGTGGCATTGATGCCCTGCCAGGGCGACAGCGGTGGTCCCTTTGTGTGTGAGGACAG 1330
Sbjct 1851  CGAGGGTGGCATTGATGCCCTGCCAGGGCGACAGCGGTGGTCCCTTTGTGTGTGAGGACAG 1910

Query 1331  CATCTCTCGGACGCCACGTTGGCGGCTGTGTGGCATTGTGAGTTGGGGCACTGGCTGTGC 1390
Sbjct 1911  CATCTCTCGGACGCCACGTTGGCGGCTGTGTGGCATTGTGAGTTGGGGCACTGGCTGTGC 1970

Query 1391  CCTGGCCCAAGAGCCAGGCGTCTACACCAAAGTCAGTGACTTCCGGGAGTGGATCTTCCA 1450
Sbjct 1971  CCTGGCCCAAGAGCCAGGCGTCTACACCAAAGTCAGTGACTTCCGGGAGTGGATCTTCCA 2030

Query 1451  GGCCATAAAGACTCACTCCGAAGCCAGCGCATGGTGACCCAGCTCTGACCGGTGGCTTC 1510
Sbjct 2031  GGCCATAAAGACTCACTCCGAAGCCAGCGCATGGTGACCCAGCTCTGACCGGTGGCTTC 2090

Query 1511  TCGTGCGCAGCCTCCAGGGCCCGAGGTGATCCCGGTGGTGGGATCCACGCTGGGCGGAG 1570
Sbjct 2091  TCGTGCGCAGCCTCCAGGGCCCGAGGTGATCCCGGTGGTGGGATCCACGCTGGGCGGAG 2150

Query 1571  GATGGGACGTTTTTCTTCTTGGGCCCGGTCCACAGGTCCAAGGACACCCTCCCTCCAGGG 1630
Sbjct 2151  GATGGGACGTTTTTCTTCTTGGGCCCGGTCCACAGGTCCAAGGACACCCTCCCTCCAGGG 2210

Query 1631  TCCTCTCTTCCACAGTGGCGGGCCCACTCAGCCCCGAGACCACCAACCTCACCTCCTG 1690
Sbjct 2211  TCCTCTCTTCCACAGTGGCGGGCCCACTCAGCCCCGAGACCACCAACCTCACCTCCTG 2270

Query 1691  ACCCCCATGTAAATATTGTTCTGCTGTCTGGGACTCCTGTCTAGGTGCCCCCTGATGATGG 1750
Sbjct 2271  ACCCCCATGTAAATATTGTTCTGCTGTCTGGGACTCCTGTCTAGGTGCCCCCTGATGATGG 2330

Query 1751  GATGCTCTTTAAATAATAAAGATGGTTTTGATT 1783
Sbjct 2331  GATGCTCTTTAAATAATAAAGATGGTTTTGATT 2363

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Score = 357 bits (193), Expect = 1e-94
 Identities = 193/193 (100%), Gaps = 0/193 (0%)
 Strand=Plus/Plus

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Query 1  TCGAGCCCGCTTTCCAGGGACCTACCTGAGGGCCACAGGTGAGGCAGCCTGGCCTAGC 60
Sbjct 1  TCGAGCCCGCTTTCCAGGGACCTACCTGAGGGCCACAGGTGAGGCAGCCTGGCCTAGC 60

Query 61  AGGCCCCACGCCACCGCCTCTGCCTCCAGGCCGCCCGCTGCTGCGGGGCCACCATGCTCC 120
Sbjct 61  AGGCCCCACGCCACCGCCTCTGCCTCCAGGCCGCCCGCTGCTGCGGGGCCACCATGCTCC 120

Query 121  TGCCCAGGCTGGAGACTGACCCGACCCCGCACTACCTCGAGGCTCCGCCCCACCTGC 180
Sbjct 121  TGCCCAGGCTGGAGACTGACCCGACCCCGCACTACCTCGAGGCTCCGCCCCACCTGC 180

Query 181  TGGACCCCAAGGGT 193
Sbjct 181  TGGACCCCAAGGGT 193

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>ref|XM_001093699.1|  PREDICTED: Macaca mulatta hepsin (transmembrane protease, serine 1), transcript variant 3 (HPN), mRNA
 Length=2363

GENE ID: 707242 HPN | hepsin (transmembrane protease, serine 1)
 [Macaca mulatta]

Sort alignments for this subject sequence by:
 E value Score Percent identity
 Query start position Subject start position

Score = 2754 bits (1491), Expect = 0.0
 Identities = 1559/1593 (97%), Gaps = 0/1593 (0%)
 Strand=Plus/Plus

Query	191	GGTCCCACCTTGCCCAAGGAGGTGACCCAGGGAATCATTAACAAGAGGCAGTGACATGGC	250
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Query	251	GCAGAAGGAGGGTGGCCGGAAGTGTGCCATGCTGCTCCAGACCCAAGGTGGCAGCTCTCAC	310
Sbjct	829	GCAGAAGGAGGGTGGCCGGAAGTGTGCCATGCTGCTCCGACCCAAGGTGGCAGCTCTCAC	888
Query	311	TGCGGGGACCTGCTACTTCTGACAGCCATCGGGGCGGCATCCTGGGCCATTGTGGCTGT	370
Sbjct	889	TGCGGGGACCTGCTACTTCTGACAGCCATCGGGGCGGCATCCTGGGCCATTGTGGCTGT	948
Query	371	TCTCCTCAGGAGTGACAGGAGCCGCTGTATCCAGTGCAGGTGAGCTCTGCGGACGCTCG	430
Sbjct	949	TCTCCTCAGGAGTGACAGGAGCCGCTGTATCCAGTGCAGGTGAGCTCTGCGGACGCTCG	1008
Query	431	GCTCATGGTCTTTGACAAGACGGAAGGACGTGGCGGCTGCTGTGCTCCTCGCGCTCCAA	490
Sbjct	1009	GCTCATGGTCTTTGACAAGACGGAAGGACGTGGCGGCTGCTATGCTCCTCACGCTCCAA	1068
Query	491	CGCCAGGGTAGCCGGAAGTCTGCTGCGAGGAGATGGGCTTCCTCAGGGCACTGACCCACTC	550
Sbjct	1069	CACCAAGGTAGCCGGAAGTCTGCTGCGAGGAGATGGGCTTCCTCAGGGCACTGACCCACTC	1128
Query	551	CGAGCTGGAGCTGCGAACCGGCGGGCGCCAATGGCAGCTCGGGCTTCTTCTGTGTGGACGA	610
Sbjct	1129	CGAGTTGGAGCTGCGAACCGGCGGGCGCCAACGGCACGTGAGGCTTCTTCTGTGTGGATGA	1188
Query	611	GGGGAGGCTGCCCCACACCCAGAGGCTGCTGGAGGTGATCTCCGTGTGTGATTGCCCCAG	670
Sbjct	1189	GGGGAGGCTGCCACACACCCAGAGGCTGCTGGAGGTGATCTCCGTGTGTGACTGTCCAG	1248
Query	671	AGGCCGTTTCTTGGCCGCCATCTGCCAAGACTGTGGCCGCGAGGAAGCTGCCCGTGGACCG	730
Sbjct	1249	AGGCCGTTTCTTGGCCACCCTTGGCAAGACTGTGGCCGCGAGGAAGCTGCCCGTGGACCG	1308
Query	731	CATCGTGGGAGGCCGGGACACAGCTTGGGCCGCTGGCCGTGGCAAGTCAAGCTTCGCTA	790
Sbjct	1309	CATCGTGGGAGGCCGGGACACAGCTTGGGCCGCTGGCCGTGGCAAGTCAAGCTTCGCTA	1368
Query	791	TGATGGAGCACACCTCTGTGGGGGATCCCTGCTCTCCGGGGACTGGGTGCTGACAGCCGC	850
Sbjct	1369	TGATGGAGCACACCTCTGCGGGGGTCCCTGCTCTCCGGGGACTGGGTGCTGACAGCTGC	1428
Query	851	CCACTGCTTCCCGAGCGGAACCGGGTCTGTCCCGATGGCGAGTGTGTCGGGTGCCGT	910
Sbjct	1429	CCACTGCTTCCCGAGCGGAACCGGGTCTGTCCCGATGGCGAGTGTGTCGGGTGCCGT	1488
Query	911	GGCCCAAGGCCTCTCCCCACGGTCTGACAGTGGGGGTGCAGGCTGTGGTCTACCAAGGGG	970
Sbjct	1489	GGCCCAAGGCCTCTCCCCACGGCCTGACAGTGGGGGTGCAGGCTGTGGTCTACCAAGGGG	1548
Query	971	CTATCTTCCCTTTCGGGACCCCAACAGCGAGGAGAACAGCAACGATATTGCCCTGGTCCA	1030
Sbjct	1549	CTATCTTCCCTTTCGGGACCCCAACAGCGAGGAGAACAGCAATGATATTGCCCTGGTCCA	1608
Query	1031	CCTCTCCAGTCCCCTGCCCCTCACAGAATACATCCAGCCTGTGTGCCTCCCAGCTGCCGG	1090
Sbjct	1609	CCTCTCCAGTCCCCTGCCCCTCACAGAATACATCCAGCCTGTGTGCCTCCCAGCTGCTGG	1668
Query	1091	CCAGGCCCTTGGTGGATGGCAAGATCTGTACCGTGACGGGCTGGGGCAACACGCAGTACTA	1150
Sbjct	1669	CCAGGCCCTTGGTGGATGGCAAGATCTGTACCGTGACGGGCTGGGGCAACACGCAGTACTA	1728
Query	1151	TGGCCAACAGGCCGGGGTACTCCAGGAGGCTCGAGTCCCATAATCAGCAATGATGTCTG	1210
Sbjct	1729	TGGCCAACAGGCCGGGGTACTCCAGGAGGCTCGAGTCCCATAATCAGCAATGATGTCTG	1788
Query	1211	CAATGGCGCTGACTTCTATGGAACAGATCAAGCCCAAGATGTTCTGTGCTGGCTACCC	1270
Sbjct	1789	CAATGGCGCTGACTTCTATGGAACAGATCAAGCCCAAGATGTTCTGTGCTGGCTACCC	1848
Query	1271	CGAGGGTGGCATTGATGCTTCCAGGGCGACAGCGGTGGTCCCTTTGTGTGTGAGGACAG	1330
Sbjct	1849	CGAGGGTGGCATTGATGCTTCCAGGGTGCAGCGGTGGTCCCTTTGTGTGTGAGGACAG	1908
Query	1331	CATCTCTCGGACGCCAGTGGCGGCTGTGTGGCATTGTGAGTTGGGGCACTGGCTGTGC	1390
Sbjct	1909	CATCTCTCGGACGCCAGTGGCGGCTGTGTGGCATTGTGAGTTGGGGCACTGGCTGTGC	1968
Query	1391	CCTGGCCCAAGAAGCCAGGCGTCTACACCAAGTCAGTGACTTCCGGGAGTGGATCTTCCA	1450
Sbjct	1969	CCTGGCCCAAGAAGCCAGGCGTCTACACCAAGTCAGTGACTTCCGGGAGTGGATCTTCCA	2028
Query	1451	GGCCATAAAGACTCACTCCGAAGCCAGCGGCATGGTGACCCAGCTCTGACCGGTGGCTTC	1510
Sbjct	2029	GGCCATAAAGACTCACTCCGAAGCCAGCGGCATGGTGACCCAGCTCTGACCGGTGGCTTC	2088
Query	1511	TCGTGCGCAGCCTCCAGGGCCCGAGGTGATCCCGGTGGTGGGATCCACGCTGGGCCGAG	1570
Sbjct	2089	TCGTGCGCAGCCTCCAGGGCCCGAGGTGATCTTGGTGGTGGGATCCACGCTGGGCCGAG	2148
Query	1571	GATGGGACGTTTTTCTTCTTGGGCCCGGTCCACAGGTCCAAGGACACCTCCCTCCAGGG	1630

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Sbjct  2149  |||||GGGACATTTTCTTCTTGGGCCCGGTCCACAGGTCCAAGGACACCCCTCCCTCCAGGG 2208
Query   1631  TCCTCTCTTCCACAGTGGCGGGCCCACTCAGCCCCGAGACCACCAACCTCACCCTCCTG 1690
Sbjct  2209  TCCTTTCTTCCACAGTGGCGGGCCCACTCAGCCCCGAGACCACCCGACCTCACCCTCCTG 2268
Query   1691  ACCCCCATGTAAATATTGTTCTGCTGTCTGGGACTCCTGTCTAGGTGCCCCTGATGATGG 1750
Sbjct  2269  ACCCCCGTGTAAATATTGTTCTGCTGTCTGGGACTCCTCTCTAGGTGCCCCTGATGACGG 2328
Query   1751  GATGCTCTTTAAATAATAAAGATGGTTTTGATT 1783
Sbjct  2329  GATGCTCTTTAAATAATAAAGATGGTTTTGATT 2361


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Score = 309 bits (167), Expect = 3e-80
 Identities = 183/191 (95%), Gaps = 0/191 (0%)
 Strand=Plus/Plus

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Query   3      GAGCCCGCTTTCCAGGGACCCCTACCTGAGGGCCCAAGGTGAGGCAGCCTGGCCTAGCAG 62
Sbjct   3      GAGCCCGCTTTCCAGGGACCCCTACCCGAGGGCCCAAGGTGAGGCAGCCTGGCCTAGCAG 62
Query   63      GCCCCACGCCACCGCCTCTGCCTCCAGGCCGCCCGCTGCTGCGGGGCCACCATGCTCCTG 122
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Sbjct   123     CCCAGGCCTGGAGACTGACCCGACCCCGGAACCACTCCAGGCTCCGCCCTCACCTGCCG 182
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>dbj|AK315655.1|  Homo sapiens cDNA, FLJ96746
 Length=1432

Score = 2645 bits (1432), Expect = 0.0
 Identities = 1432/1432 (100%), Gaps = 0/1432 (0%)
 Strand=Plus/Plus

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Query   128     GCCTGGAGACTGACCCGACCCCGGCACTACCTCGAGGCTCCGCCCCACCTGCTGGACCC 187
Sbjct   61      GCCTGGAGACTGACCCGACCCCGGCACTACCTCGAGGCTCCGCCCCACCTGCTGGACCC 120
Query   188     CAGGGTCCCACCTGGCCCAGGAGGTCAGCCAGGGAATCATTAAAGAGGCAGTGACAT 247
Sbjct   121     CAGGGTCCCACCTGGCCCAGGAGGTCAGCCAGGGAATCATTAAAGAGGCAGTGACAT 180
Query   248     GGCGCAGAAAGGAGGGTGGCCGGAAGTGTGCTGCTCCAGACCCAGGTGGCAGCTCT 307
Sbjct   181     GGCGCAGAAAGGAGGGTGGCCGGAAGTGTGCTGCTCCAGACCCAGGTGGCAGCTCT 240
Query   308     CACTGCGGGGACCTGTACTTCTGACAGCCATCGGGGCGGCATCCTGGGCCATTGTGGC 367
Sbjct   241     CACTGCGGGGACCTGTACTTCTGACAGCCATCGGGGCGGCATCCTGGGCCATTGTGGC 300
Query   368     TGTTCCTCTCAGGAGTGACAGGAGCCGCTGTACCCAGTGACAGGTGAGCTCTGCGGACGC 427
Sbjct   301     TGTTCCTCTCAGGAGTGACAGGAGCCGCTGTACCCAGTGACAGGTGAGCTCTGCGGACGC 360
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Query   488     CAACGCCAGGGTAGCCGGAAGTCACTGCGAGGAGATGGGCTTCTCAGGGCACTGACCCA 547
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Query   728     CCGCATCGTGGGAGGCCGGGACACAGCTTGGGCCGGTGGCCGTGGCAAGTCAGCCTTCG 787
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Query   788     CTATGATGGAGCACACCTCTGTGGGGGATCCCTGCTCTCCGGGGAAGTGGGTGCTGACAGC 847
Sbjct   721     CTATGATGGAGCACACCTCTGTGGGGGATCCCTGCTCTCCGGGGAAGTGGGTGCTGACAGC 780
Query   848     CGCCCACTGCTTCCCGAGCGGAACCGGGTCTGTCCCGATGGCGAGTGTTTGCCGGTGC 907

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Sbjct  781  |||||CAGTCTTCCCGAGCGGAACCGGGTCTGTCCCGATGGCGAGTGTGTTGCCGGTGC 840
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Sbjct  841  CGTGGCCAGGCTCTCCCCACGGTCTGCAGCTGGGGGTGCAGGCTGTGGTCTACCACGG 900
Query  968  GGGTATCTTCCCTTTTCGGGACCCCAACAGCGAGGAGAACAGCAACGATATTGCCCTGGT 1027
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Query  1028  CCACCTCTCCAGTCCCCCTGCCCTCACAGAATACATCCAGCCTGTGTGCCTCCCAGCTGC 1087
Sbjct  961  CCACCTCTCCAGTCCCCCTGCCCTCACAGAATACATCCAGCCTGTGTGCCTCCCAGCTGC 1020
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Sbjct  1321  TGCCCTGGCCAGAAAGCCAGGCGTCTACACCAAAGTCAGTGACTTCCGGGAGTGGATCTT 1380
Query  1448  CCAGGCCATAAAGACTCACTCCGAAGCCAGCGGCATGGTGACCCAGCTCTGA 1499
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>gb|DQ895314.2|  Synthetic construct Homo sapiens clone IMAGE:100009774; FLH183201.01L; RZPDo839H04139D hepsin (transmembrane protease, serine 1) (HPN) gene, encodes complete protein
Length=1294

GENE ID: 3249 HPN | hepsin (transmembrane protease, serine 1) [Homo sapiens]
(Over 10 PubMed links)


Score = 2309 bits (1250), Expect = 0.0
Identities = 1252/1253 (99%), Gaps = 0/1253 (0%)
Strand=Plus/Plus

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Query  365  GGCTGTTTCTCCTCAGGAGTGACCAGGAGCCGCTGTACCCAGTGCAGGTGAGCTCTGCGGA 424
Sbjct  142  GGCTGTTTCTCCTCAGGAGTGACCAGGAGCCGCTGTACCCAGTGCAGGTGAGCTCTGCGGA 201
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Sbjct  382  GGACGAGGGGAGGCTGCCCCACACCAGAGGCTGTGGAGGTGATCTCCGTGTGTGATTG 441
Query  665  CCCAGAGGCGGTTTCTTGGCCGCCATCTGCCAAGACTGTGGCCGAGGAAGCTGCCCCGT 724
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Query  725  GGACCGCATCGTGGGAGGCCGGGACACCAGCTTGGGCCGGTGGCCGTGGCAAGTCAGCCT 784
Sbjct  502  GGACCGCATCGTGGGAGGCCGGGACACCAGCTTGGGCCGGTGGCCGTGGCAAGTCAGCCT 561
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Sbjct  562  TCGTATGATGGAGCACACCTCTGTGGGGATCCCTGCTCTCCGGGACTGGGTGCTGAC 621
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Sbjct 682  TGCCGTGGCCAGGCGCTCTCCACCGGTCTGCAGCTGGGGGTGCAGGCTGTGGTCTACCA 741
Query 965  CGGGGGCTATCTTCCCTTTTCGGGACCCCAACAGCGAGGAGAACAGCAACGATATTGCCCT 1024
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>gb|DQ892119.2|  Synthetic construct clone IMAGE:100004749; FLH183205.01X; RZPD0839H04140D
hepsin (transmembrane protease, serine 1) (HPN)
gene, encodes complete protein
Length=1294

GENE ID: 3249 HPN | hepsin (transmembrane protease, serine 1) [Homo sapiens]
(Over 10 PubMed links)

Score = 2309 bits (1250), Expect = 0.0
Identities = 1252/1253 (99%), Gaps = 0/1253 (0%)
Strand=Plus/Plus

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Query 245  CATGGCGCAGAAAGGAGGGTGGCCGACTGTGCCATGCTGCTCCAGACCCAAGGTGGCAGC 304
Sbjct 22  CATGGCGCAGAAAGGAGGGTGGCCGACTGTGCCATGCTGCTCCAGACCCAAGGTGGCAGC 81
Query 305  TCTCACTGCGGGGACCTTGCTACTTCTGACAGCCATCGGGGCGGCATCCTGGGCCATTGT 364
Sbjct 82  TCTCACTGCGGGGACCTTGCTACTTCTGACAGCCATCGGGGCGGCATCCTGGGCCATTGT 141
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Query 725  GGACCGCATCGTGGGAGGCCGGGACACCAGCTTGGGCCGGTGGCCGTGGCAAGTCAGCCT 784
Sbjct 502  GGACCGCATCGTGGGAGGCCGGGACACCAGCTTGGGCCGGTGGCCGTGGCAAGTCAGCCT 561
Query 785  TCGTATGATGGAGCACACCTCTGTGGGGATCCCTGCTCTCCGGGACTGGGTGCTGAC 844
Sbjct 562  TCGTATGATGGAGCACACCTCTGTGGGGATCCCTGCTCTCCGGGACTGGGTGCTGAC 621
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Sbjct	622	AGCCGCCCATTGCTTCCCGGAGCGGAACCGGGTCTCTGCCGATGGCGAGTGTTTGCCGG	681
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Sbjct	682	TGCCGTGGCCAGGCGCTCTCCCCACGGTCTGCAGCTGGGGGTGCAGGCTGTGGTCTACCA	741
Query	965	CGGGGGCTATCTTCCTTTTCGGGACCCCAACAGCGAGGAGAACAGCAACGATATTGCCCT	1024
Sbjct	742	CGGGGGCTATCTTCCTTTTCGGGACCCCAACAGCGAGGAGAACAGCAACGATATTGCCCT	801
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>gb|EU644753.1| Homo sapiens truncated hepsin serine protease mRNA, complete
cds
Length=1209
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Score = 2228 bits (1206), Expect = 0.0
Identities = 1206/1206 (100%), Gaps = 0/1206 (0%)
Strand=Plus/Plus

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Query	306	CTCACTGCGGGGACCCCTGCTACTTCTGACAGCCATCGGGGCGGCATCCTGGGCCATTGTG		365
Sbjct	61	CTCACTGCGGGGACCCCTGCTACTTCTGACAGCCATCGGGGCGGCATCCTGGGCCATTGTG		120
Query	366	GCTGTTCTCCTCAGGAGTGACCAGGAGCCGCTGTACCCAGTGCAAGGTACAGCTCTGCGGAC		425
Sbjct	121	GCTGTTCTCCTCAGGAGTGACCAGGAGCCGCTGTACCCAGTGCAAGGTACAGCTCTGCGGAC		180
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Sbjct	361	GACGAGGGGAGGCTGCCCCACACCCAGAGGCTGCTGGAGGTATCTCCGTGTGTGATTGC		420
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Sbjct	421	CCAGAGGCCGTTCTTGGCCGCCATCTGCCAAGACTGTGGCCGAGGAAGCTGCCCGTG		480
Query	726	GACCGCATCGTGGGAGGCCGGGACACAGCTTGGGCCGGTGGCCGTGGCAAGTCAGCCTT		785
Sbjct	481	GACCGCATCGTGGGAGGCCGGGACACAGCTTGGGCCGGTGGCCGTGGCAAGTCAGCCTT		540
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>emb|X07002.1|HSHPEPSL  H.sapiens liver mRNA for serine protease hepsin
Length=1199

GENE ID: 3249 HPN | hepsin (transmembrane protease, serine 1) [Homo sapiens]
(Over 10 PubMed links)

Score = 2215 bits (1199), Expect = 0.0
Identities = 1199/1199 (100%), Gaps = 0/1199 (0%)
Strand=Plus/Plus

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Query 645 GTCATCTCCGTGTGTGATTGCCCCAGAGGCCGTTTCTTGGCCGCCATCTGCCAAGACTGT 704
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Query 705 GGCCGCGAGGAAGCTGCCCGTGGACCGCATCGTGGGAGGCCGGGACACCAGCTTGGGCCGG 764
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Query 765 TGGCCGTGGCAAGTCAGCCTTCGCTATGATGGAGCACACCTCTGTGGGGGATCCCTGCTC 824
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Sbjct 541 ACGGGCTGGGGCAACACGCAGTACTATGGCCAAACAGGCCGGGGTACTCCAGGAGGCTCGA 600
Query 1185 GTCCCCATAATCAGCAATGATGTCTGCAATGGCGCTGACTTCTATGGAAACAGATCAAG 1244
Sbjct 601 GTCCCCATAATCAGCAATGATGTCTGCAATGGCGCTGACTTCTATGGAAACAGATCAAG 660
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Query 1305  GGTGGTCCCTTTGTGTGTGAGGACAGCATCTCTCGGACGCCACGTTGGCGGCTGTGTGGC 1364
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Query 1365  ATTGTGAGTTGGGGCACTGGCTGTGCCCTGGCCAGAAAGCCAGGCGTCTACACCAAAGTC 1424
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Query 1425  AGTGACTTCCGGGAGTGGATCTTCCAGGCCATAAAGACTCACTCCGAAGCCAGCGGCATG 1484
Sbjct 841    AGTGACTTCCGGGAGTGGATCTTCCAGGCCATAAAGACTCACTCCGAAGCCAGCGGCATG 900

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Sbjct 901    GTGACCCAGCTCTGACCGGTGGCTTCTCGCTGCGCAGCCTCCAGGGCCCGAGGTGATCCC 960


Query 1545  GGTGGTGGGATCCACGCTGGGCCGAGGATGGGACGTTTTTCTTCTTGGGCCCGGTCCACA 1604
Sbjct 961    GGTGGTGGGATCCACGCTGGGCCGAGGATGGGACGTTTTTCTTCTTGGGCCCGGTCCACA 1020

Query 1605  GGTCCAAGGACACCCCTCCCTCCAGGGTCTCTCTTCCACAGTGGCGGGCCCACTCAGCCC 1664
Sbjct 1021   GGTCCAAGGACACCCCTCCCTCCAGGGTCTCTCTTCCACAGTGGCGGGCCCACTCAGCCC 1080

Query 1665  CGAGACCACCCAACTCACCTCCTGACCCCCATGTAAATATTGTTCTGCTGTCTGGGAC 1724
Sbjct 1081   CGAGACCACCCAACTCACCTCCTGACCCCCATGTAAATATTGTTCTGCTGTCTGGGAC 1140

Query 1725  TCCTGTCTAGGTGCCCCGTGATGATGGGATGCTCTTTAAATAATAAAGATGGTTTTGATT 1783
Sbjct 1141   TCCTGTCTAGGTGCCCCGTGATGATGGGATGCTCTTTAAATAATAAAGATGGTTTTGATT 1199

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>dbj|AK233353.1|  Sus scrofa mRNA, clone:LVRM10127D02, expressed in liver
Length=1785

Score = 2069 bits (1120), Expect = 0.0
Identities = 1547/1750 (88%), Gaps = 42/1750 (2%)
Strand=Plus/Plus

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Query 66     CCACGCCACCGCCTCTGCCTCC-AGGCCGCCCCGCTGCTGCGGGGCCACCATGCTCCTGCC 124
Sbjct 21     CCAC-CCGCTGCCTCTGCCTCCGGGGCC-TCCGCCGCTGCGGGGCCACCGTGCTCCTGCC 78

Query 125    CAGGCCTGGAGACTGA-CCC-GACCCCGGCA-C-TACCTCGAGGCTCCGCCCCACCTGC 180
Sbjct 79     CAGGCCTGGAGACTGACCCCTAAACCCGGCACCGTGTCTC-A-GCTCTGCCCCACCCGC 136

Query 181    TGGACCCAGGGTCCCACCTGGCCAGGAGGTGAGCCAGGGAATCATTAACAAGAGGCA 240
Sbjct 137    CGGACCCAGGGTCCCGCCCCGGCCAGGAGGTGAGCCGGGGATCATTAAGTAGAGGCC 196

Query 241    GTGACATGGCGCAGAAGGAGGTGGCCGACTGTGCCATGCTGCTCCAGACCCAAGGTGG 300
Sbjct 197    GTGACATGGCGGAGAAAGAGGTGGCCAGCCTGTGTCTGCTGCTCCGGACCCAAGGTGG 256

Query 301    CAGCTCTCACTGCGGGGACCCTGCTACTTCTGACAGCCATCGGGGCGGCATCCTGGGCCA 360
Sbjct 257    CAGCTCTCACTGTGGGGACCGTGCTGCTCCTGACAGGCATTGGGGCAGCGTCTGGGCCA 316

Query 361    TTGTGGCTGTCTCTCCTCAGGAGTGACAGGAGCCGCTGTACCCAGTGCAGGTGAGCTCTG 420
Sbjct 317    TTGTGACCGTTCTACTCAGGAGTGATCAGGAGCCGCTGTATCCAGTGCAGGTGCGCCCCG 376

Query 421    CGGACGCTCGGCTCATGGTCTTTGACAAGACGGAAGGG-ACGTGGCGGCTGCTGTGCTCC 479
Sbjct 377    GGGATTCTCGGCTCACCGTGTGTGATGAGACGG-AGGGCACGTGGCGCCTGCTGTGCTCC 435

Query 480    TCGCGCTCCAACGCCAGGGTAGCCGACTCAGCTGCGAGGAGATGGGCTTCCTCAGGGCA 539
Sbjct 436    TCGCGCTCCAACGCCAGGGTGGCAGGGCTCAGCTGCGAGGAGATGGGCTTCCTCAGGTCA 495

Query 540    CTGACCCACTCCGAGCTGGACGTGCGAACGCGGGCGCCAATGGCAGTCCGGGCTTCTTC 599
Sbjct 496    CTGACCCACTCAGAGCTGGATGTGCGGACTGCGGGCGCCAACGGCACGTCCGGGCTTCTTC 555

Query 600    TGTGTGGACGAGGGGAGGCTGCCCCACACCCAGAGGCTGCTGGAGGTGATCTCCGTGTGT 659
Sbjct 556    TGTGTGGATGAGGGGAGGCTGCCGACGGCCCGGAGGCTGCTTGAGGTCTCTCTGTGTGC 615

Query 660    GATTGCCCCAGAGGCCGTTTCTTGGCCGCCATC-TGCCAAGACTGTGGCCGCAGGAAGCT 718
Sbjct 616    GACTGTCCCAGGGGCCATTTCTGGCAACCA-CATGCCAAGACTGCGGCCATAGGAAGCT 674

Query 719    GCCCGTGGACCGCATCGTGGGAGGCGGGACACAGCTTGGGCGGCTGGCCGTGGCAAGT 778
Sbjct 675    GCCCGTGGATCGCATTTGTGGGCGGTGAGGACACAGCCTGGGCGGCTGGCCGTGGCAAGT 734

Query 779    CAGCCTTCGCTATGATGGAGCACACCTCTGTGGGGATCCCTGCTCTCCGGGACTGGGT 838
Sbjct 735    CAGTCTTCGCTACGACGGAGCACACCTCTGTGGGGATCCCTGCTCTCCAAGACTGGGT 794

Query 839    GCTGACAGCCGCCCACTGCTTCCCAGGAGCGGAACCGGGTCTGTCCCAGTGGCGAGTGTT 898
Sbjct 795    GCTGACAGCCGCCCACTGCTTCCCAGGAGCGGAACCGGGTCTGTCTCGATGGCGAGTATT 854



Query 899    TGCCGGTGGCGTGGCCAGGCCTCTCCCCACGGTCTGCAGCTGGGGGTGCAGGCTGTGGT 958

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Sbjct  855  CGCCGGTGTCTGTGGCCAGACCTCAACCCACGGCTGCAGATGGGGGTGCAGGCGGTGAT  914
Query  959  CTACCACGGGGCTATCTTCCCTTTTCGGGACCCCAACAGCGAGGAGAACAGCAACGATAT  1018
Sbjct  915  CTACCATGGGGACTATCTCCCTTTTCGAGACCCCAACAGTGAGGAGAACAGCAATGATAT  974
Query  1019  TGCCCTGGTCCACCTCTCCAG-TCCCTGCCCCCTACAGAATACATCCAGCCTGTGTGCC  1077
Sbjct  975  CGCCCTGGTCCACCTCTCCAGCTCCC-TGGTCTCACAAGAATACATCCAGCCTGTGTGCC  1033
Query  1078  TCCAGCTGCGCGCCAGGCCCTGGTGGATGGCAAGATCTGTACCGTGACGGGCTGGGGCA  1137
Sbjct  1034  TCCCGGCTGCGCGCCAAGCCCTGGTGGACGGCAAGATCTGCACGGTGACAGGCTGGGGCA  1093
Query  1138  ACACGCAGTACTATGGCCAACAGGCCGGGGTACTCCAGGAGGCTCGAGTCCCCATAATCA  1197
Sbjct  1094  ACACGCAGTACTATCGGCCAACAGGCTGGGGTGCTCCAGGAGGCCCGAGTCCCCATAATCA  1153
Query  1198  GCAATGATGTCTGCAATGGCGCTGACTTCTATGGAAACAGATCAAGCCCAAGATGTTCT  1257
Sbjct  1154  GCAATGATGTCTGCAATGGCCCCGACTTCTACGGAAACAGATCAAGCCCAAGATGTTCT  1213
Query  1258  GTGCTGGCTACCCCGAGGGTGGCATTGATGCCTGCCAGGGCGACAGCGGTGGTCCCTTTG  1317
Sbjct  1214  GTGCCGGCTACCCCTGAGGGTGGCATTGACGCCTGCCAGGGTGACAGTGGTGGCCCTTCG  1273
Query  1318  TGTGTGAGGACAGCATCTCTCGGACGCCACGTTGGCGGCTGTGTGGCATTGTGAGTTGGG  1377
Sbjct  1274  TGTGTGAGGACAGCATCTCTCGGACGCCACGTTGGCGGCTGTGTGGCATCGTGAGCTGGG  1333
Query  1378  GCACTGGCTGTGCCCTGGCCAGAAGCCAGGCGTCTACACCAAAGTCAGTGACTTCCGGG  1437
Sbjct  1334  GCACCGGCTGTGCCCTGGCCAAAAGCCAGGCGTCTACACCAAAGTCAGTGACTTCCGGG  1393
Query  1438  AGTGGATCTTCCAGGCCATAAAGACTCACTCCGAAGCCAGCGCATGGTGACCCAGCTCT  1497
Sbjct  1394  AGTGGATCTTCCAGGCCATAAAGACTCACTCCGAAGCCAGCGCATGGTGACCCAGCTCT  1453
Query  1498  GACCGGTGGCTTCT-C--GCTGCGCA-GCCTCCAGGGCCCGAGGTGATCCCGGTGG-TG-  1551
Sbjct  1454  GACCTGCGGCTTCTGCTCGCTGCGCTCGCCTCCAGGGCCCAAGCTGATCCAGGTGGCTCC  1513
Query  1552  -G-----GATC-----CACGCTGGGCC-GAGGATGGGACGTTTTTCTTCTTGGGCC  1596
Sbjct  1514  AGCCCTCATGATGGGGTTCACCCCTGGGCTG-GGATAGAACATTTTTCTTCTTGGGCC  1572
Query  1597  GGTCCACAGGTCCAAGGACACCTCCCTCCAGGGTCTCTCTTCCACAGTGGCGGGCCCA  1656
Sbjct  1573  AGCCCAACAGGTCCAAGGATACCCCTCCCTCCAAGGTCTCTCTTCCACAGTGGCGGGCCCA  1632
Query  1657  CTCAGCCCCAG-ACCACCCAA-CCTCACCTCCTGACCCCCATGTAAATATTGTTCTGC  1714
Sbjct  1633  CTCAGCCCTG-GCATCACCCGAGCCTCACCTCCTGACCCCCATGTAAATATTGTTCTGC  1691
Query  1715  TGTCTGGGA-CTCCTGTCTAGGTGCCCTGATGATGGGATGCTCTTTAAATAATAAAGAT  1773
Sbjct  1692  CATCTGGGGGCCCTATCTAG-TGCCCTGATGACAGGATGCTCTTTAAATAATAAAGAT  1750
Query  1774  GGTTTTGATT 1783
Sbjct  1751  GGTTTTGATT 1760

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>ref|NM_001080241.2|  Bos taurus hepsin (transmembrane protease, serine 1) (HPN), mRNA
gb|BC140636.1|  Bos taurus hepsin (transmembrane protease, serine 1), mRNA (cDNA clone MGC:148484 IMAGE:8196479), complete cds
Length=1919

GENE ID: 508148 HPN | hepsin (transmembrane protease, serine 1) [Bos taurus]
(10 or fewer PubMed links)

Score = 1973 bits (1068), Expect = 0.0
Identities = 1552/1777 (87%), Gaps = 67/1777 (3%)
Strand=Plus/Plus

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Query  49  GCCTGGCCTAGCAGGCCCCACGC-CA-CCGC--C-TCTGCCTCCAGGCC-GCCCGCTGCT  102
Sbjct  2    GCCAGGCCTAGCAGGCCCTCGCGCTGCCGCTGCCTCTGCCTCC-GGCCCGCTGCGCT  60
Query  103  GCGGGGCCACCATGCTCCTGCCAGGCCTGGAGACTGACCCGAC-CCCGGCACTA-C-CT  159
Sbjct  61    GCGGGGCCACCATGCTCCTGCCAGGCCTGGAGACTGACCTAAACCCG-CACCATCTCT  119
Query  160  CGAGGCTCCGCCCCACCTGCTGGAACCCAGGGTCCCACCTGGCCAGGAGGTGAGCCA  219
Sbjct  120  C-AG-CTCCGCCCCACCTGCGGACCCAGGGTCCCGCCCCGGCCCGGAGGTGAGCCG  177
Query  220  GGGGAATCATTAACAAGAGGCAGTGACATGGCGCAGAAGGAGGGTGGCCGACTGTGCCAT  279
Sbjct  178  GGGGAATCATTAAGTAGAGGCTGTGACATGGCGGAGAAGGAGGGTGGCCGACTGTGCCAT  237
Query  280  GCTGCTCCAGACCCAAGGTGGCAGCTCTCACTGCGGGGACCCTGCTACTTCTGACAGCCA  339
Sbjct  238  GCTGCTCCGACCCAAGGTGGCCGCTCTCACTGTGGGGACCGTCTGCTCCTGACAGGCA  297
Query  340  TCGGGGCGGCATCCTGGGCCATTGTGGCTGTTCTCCTCAGGAGTGACCAGGAGCCGCTGT  399

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Sbjct  298      TCGGGGCAGCGTCTCTGGGCCATTGTGACTGTTCTACTCAGGAGTGATCAGGAGCCACTGT 357
Query  400      ACCCAGTGCAGGTCTGCGGACGCTCGGCTCATGGTCTTTGACAAGACGGAAGGG - 458
Sbjct  358      ATCCAGTGCAGGTCTGGCCCCGCGGATGCTCGGCTCACGGTGTTTCGACCAGACAGA -GGGC 416
Query  459      ACGTGGCGGCTGCTGTGCTCCTCGCGCTCCAACGCGAGGGTAGCCGGACTCAGCTGCGAG 518
Sbjct  417      ACGTGGCGCCTGCTTTGCTCCTCGCGCTCCAATGCCAGGGTGGCGGGGCTCAGCTGCGAG 476
Query  519      GAGATGGGCTTCTCTCAGGGCACTG-ACCCACTCCGAGCTGGACGTGCGAACGGCGGGCGC 577
Sbjct  477      GAGATGGGCTTCTCTCAGGGCGTTGGACTT-CTCGGAGCTGGACGTGCGGACGGCGGGCGC 535
Query  578      CAATGGCACGTCGGGCTTCTTCTGTGTGGACGAGGGGAGGCTGCCCCACACCAGAGGCT 637
Sbjct  536      CAATGGCACGTCGGGCTTCTTCTGCGTGGACGAGGGGAGGCTGCCCGATGCCCGGAGGTT 595
Query  638      GCTGGAGGTCATCTCCGTGTGTGATGCCCCAGAGGCCGTTTCTTGGCCGCCATCTGCCA 697
Sbjct  596      GCTCGAGGTCCTCTCCGTGTGCGACTGTCCCAGAGGCCGTTTCTTGCTACCAGCTGCCA 655
Query  698      AGACTGTGGCCGCGAGGAAGCTGCCCGTGGACCGCATCGTGGGAGGCCGGGACACCAGCTT 757
Sbjct  656      AGACTGTGGCCACCGAAACTGCCCGTCGATCGCATTGTGGGCGGCCAGGACACCAGCCT 715
Query  758      GGGCCGGTGGCCGTGGCAAGTCAGCCTTCGCTATGATGGAGCACACCTCTGTGGGGGATC 817
Sbjct  716      GGGCAGGTGGCCGTGGCAAGTCAGTCTTCGCTATGATGGAGCACATCTCTGTGGGGGGTC 775
Query  818      CCTGCTCTCCGGGGACTGGGTGCTGACAGCCGCCACTGCTTCCCGGAGCGGAACCGGGT 877
Sbjct  776      CGTGCTCTCTAGGGACTGGGTGCTGACAGCCGCCACTGCTTCCCTGAGCGGAACCGGGT 835
Query  878      CCTGTCCCAGTGGCGAGTGTGTTGCCGGTGCCGTGGCCAGGCCTCTCCCACGGTC-TGC 936
Sbjct  836      CCTATCAGATGGCGAGTGTGTTGCTGGTGCTGTGGCCAGACTTCACCCCATGG-CGTGC 894
Query  937      AGCTGGGGGTGCAAGGCTGTGGTCTACACGGGGGCTATCTTCCCTTTGCGGACCCCAACA 996
Sbjct  895      AACTGGGGGTGCAAGGCTGTCTCTACCATGGGGGCTATCTCCCTTTTCAGACCCCAACA 954
Query  997      GCGAGGAGAAACAGCAACGATATTGCCCTGGTCCACCTCTCCAGTC-CCCTGCCCCTCACA 1055
Sbjct  955      GCGAGGAGAAATAGCAATGACATCGCCCTGGTCCACCTCTCCGG-CACCCTGCCCCTCACA 1013
Query  1056     GAATACATCCAGCCTGTGTGCCTCCAGCTGCCGGCCAGGCCCTGGTGGATGGCAAGATC 1115
Sbjct  1014     GAGTACATCCAGCCCGTGTGTCTCCCGGCTGCCGGGCAGGCCCTGGTGGATGGCAAGATC 1073
Query  1116     TGTACCGTGACGGGCTGGGGCAACACGCAGTACTATGGCCAACAGGCCGGGGTACTCCAG 1175
Sbjct  1074     TGCACGGTGACTGGCTGGGGCAACACGCAGTACTACGGCCAACAGGCTGGGGTGCTCCAG 1133
Query  1176     GAGGCTCGAGTCCCCATAATCAGCAATGATGTCTGCAATGGCGCTGACTTCTATGGAAAC 1235
Sbjct  1134     GAGGCCCGAGTCCCCATAATCAGCAATGATGTCTGCAACGGCCCCGACTTCTACGGGAAC 1193
Query  1236     CAGATCAAGCCCCAAGATGTTCTGTGCTGGCTACCCGAGGGTGGCATTGATGCCTGCCAG 1295
Sbjct  1194     CAGATCAAGCCCCAAGATGTTCTGTGCTGGCTACCTGAGGGTGGCATTGATGCCTGCCAG 1253
Query  1296     GGGACACAGCGGTGGTCCCTTTGTGTGTGAGGACAGCATCTCTCGGACGCCACGTTGGCGG 1355
Sbjct  1254     GGGACACAGTGGTGGCCCCCTTCGTGTGTGAGGATAGCATCTCTCGGACGCCACGTTGGCGG 1313
Query  1356     CTGTGTGGCATTGTGAGTTGGGGCACTGGCTGTGCCCTGGCCAGAAGCCAGGCGTCTAC 1415
Sbjct  1314     CTGTGTGGCATTGTGAGCTGGGGCACCGGCTGTGCCCTGGCCAGAAGCCAGGCGTCTAC 1373
Query  1416     ACCAAAGTCAGTGACTTCCGGGAGTGGATCTTCCAGGCCATAAAGACTCACTCCGAAGCC 1475
Sbjct  1374     ACCAAAGTCAGTGACTTCCGGGAGTGGATCTTCCAGGCCATAAAGACTCACTCCGAAGCC 1433
Query  1476     AGCGGCATGGTGACCCAGCTCTGACCGGTGGCTTCTC---GCTGCGCA-GCCTCCAGGGC 1531
Sbjct  1434     AGCGGCATGGTAACCCAGCTTTGACCTGTGGCTTCTCCTCGCTGTGCACGCTCCAGGGC 1493
Query  1532     CCGAGGTGATC-----CC---G-----GTGGTGGGATCCACGCTGGGCCGAGG-ATG 1574
Sbjct  1494     CCGAGCTGATCTAAGGGGCCCCAGCCCCACGTGATGGGGTTCACCTGGGGC-AGGGATG 1552
Query  1575     GGACGTTTTTCTTCTTGGGCCCGGTCCACAGGTCCAAGGACACCCCT-CCCTCCAGGGTCC 1633
Sbjct  1553     GAACATTTTTCTTCTTGGGCCAGCCACAGGTCCAAGGATACTCTTCCCTCCAAGGTCC 1612
Query  1634     TCTCTTCCACAGTGGCGGGCCCACTCAGCCCCGAGACCACCCAACTCACCTCCTGACC 1693
Sbjct  1613     TC-C---ACAGTGGCGGGCCCACTCAGCCCTGGGACCAACC---TC-C---TGC---CC 1657
Query  1694     CCCATGTAAATATTGTTCTGCTGTCTGGGA-CTCTG-----TCTAGGTGCCCTGATG 1746
Sbjct  1658     CCCATGTAAATATTGTTCTGCCATCTGGGATCCCCCCCCCATCTTG-TGCTCCTGAAG 1716
Query  1747     ATGGGATGCTCTTTAAATAATAAAGATGGTTTTTGATT 1783
Sbjct  1717     ACAGGATGCTCTTTAAATAATAAAGATGGTTTTTGATT 1753

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>gb|BT029913.1|  Bos taurus hepsin (transmembrane protease, serine 1) (HPN), mRNA, complete cds
Length=1704

GENE ID: 508148 HPN | hepsin (transmembrane protease, serine 1) [Bos taurus]
(10 or fewer PubMed links)

Score = 1956 bits (1059), Expect = 0.0
Identities = 1514/1727 (87%), Gaps = 58/1727 (3%)
Strand=Plus/Plus

Query	91	CCGCCCCGTGCTGCGGGGCCACCATGCTCCTGCCAGGCCTGGAGACTGACCC-GACCCC	149
Sbjct	2	CCGCTGTGCTGCTGCGGGGCCACCATGCTCCTGCCAGGCCTGGAGACTGACCTAAACCC	61
Query	150	GGCACTA-C-CTCAGGCTCCGCCCCACCTGCTGGACCCAGGGTCCACCTGGCCCA	207
Sbjct	62	-GCACCTCTCTC-A-GCTCCGCCCCACCTGCCGGAACCCAGGGTCCGCCCCGGCCCC	118
Query	208	GGAGGTGAGCCAGGGAATCATTAAACAGAGGCAGTGACATGGCGCAGAAGGAGGGTGGCC	267
Sbjct	119	GGAGGTGAGCCGGGGAATCATTAACTAGAGGCTGTGACATGGCGGAGAAGGAGGGTGGCC	178
Query	268	GGACTGTGCCATGCTGCTCCAGACCAAGGTGGCAGCTCTCACTGCGGGGACCTGCTAC	327
Sbjct	179	GGACTGTGCCATGCTGCTCCGGAACCAAGGTGGCGCTCTCACTGTGGGACCGTCTGC	238
Query	328	TTCTGACAGCCATCGGGGCGGCATCTGGGCCATTGTGGCTGTTCTCCTCAGGAGTGACC	387
Sbjct	239	TCCTGACAGGCATCGGGGCGAGCTCTGGGCCATTGTGACTGTTCTACTCAGGAGTGATC	298
Query	388	AGGAGCCGCTGTACCCAGTGCAAGTGCAGCTCTGCGGACGCTCGGCTCATGGTCTTTGACA	447
Sbjct	299	AGGAGCCACTGTATCCAGTGCAAGTGCAGCTCGGCCGCGGATGCTCGGCTCACGGTGTTCGACC	358
Query	448	AGACGGAAGGG-ACGTGGCGGTGCTGTGCTCCTCGCGCTCCAACGCCAGGGTAGCCGGA	506
Sbjct	359	AGACAGA-GGGCACGTGGCGCTGCTTTGCTCCTCGCGCTCCAATGCCAGGGTGGCGGG	417
Query	507	CTCAGCTGCGAGGAGATGGGCTTCTCAGGGCACTG-ACCCACTCCGAGCTGGACGTGCG	565
Sbjct	418	CTCAGCTGCGAGGAGATGGGCTTCTCAGGGCGTTGGACTT-CTCGGAGCTGGACGTGCG	476
Query	566	AACGGCGGGCGCAATGGCACGTCGGGCTTCTTCTGTGTGGACGAGGGGAGGCTGCCCCA	625
Sbjct	477	GACGGCAGGCGCCAATGGCACGTCGGGCTTCTTCTGCGTGGACGAGGGGAGGCTGCCGCA	536
Query	626	CACCAGAGGCTGCTGGAGGTCACTCCGTGTGTGATTGCCCCAGAGGCCGTTTCTGGC	685
Sbjct	537	TGCCCGAGGTTGCTCGAGGTCTCTCCGTGTGCGACTGTCCAGAGGCCGTTTCTGGC	596
Query	686	CGCCATCTGCCAAGACTGTGGCCGAGGAAGCTGCCCCGTGGACCGCATCGTGGGAGGCCG	745
Sbjct	597	TACCAGCTGCCAAGACTGTGGCCACCGAAACTGCCGGTCGATCGCATTGTGGGCGGCCA	656
Query	746	GGACACCAGCTTGGGCCGCTGGCCGTGGCAAGTCAGCCTTCGCTATGATGGAGCACACT	805
Sbjct	657	GGACACCAGCCTGGGCAGGTGGCCGTGGCAAGTCAGTCTTCGCTATGATGGAGCACATCT	716
Query	806	CTGTGGGGGATCCCTGCTCTCCGGGACTGGGTGCTGACAGCCGCCCACTGCTTCCCGGA	865
Sbjct	717	CTGTGGGGGTCCTGCTCTTAGGACTGGGTGCTGACAGCCGCCCACTGCTTCCCTGA	776
Query	866	GCGGAACCGGGTCTGTCCCAGTGGCGAGTGTGTCGGGTGCGGTGGCCAGGCCCTCTCC	925
Sbjct	777	GCGGAACCGGGTCTGTACGATGGCGAGTGTGTCGGGTGCTGTGGCCAGACTTCACC	836
Query	926	CCACGGTC-TGCAGCTGGGGGTGCAGGCTGTGGTCTACCACGGGGGCTATCTCCCTTTC	984
Sbjct	837	CCATGG-CGTGCAACTGGGGGTGCAGGCTGTCACTACCATGGGGGCTATCTCCCTTTC	895
Query	985	GGGACCCCAACAGCGAGGAGAACAGCAACGATATTGCCCTGGTCCACCTCTCCAGTC-CC	1043
Sbjct	896	GAGACCCCAACAGCGAGGAGAAAGCAATGACATCGCCCTGGTCCACCTCTCCGG-CACC	954
Query	1044	CTGCCCCCTACAGAATACATCCAGCCTGTGTGCCTCCAGCTGCCGGCCAGGCCCTGGTG	1103
Sbjct	955	CTGCCCCCTACAGAGTACATCCAGCCCGTGTGTCTCCGGCTGCCGGGAGGCCCTGGTG	1014
Query	1104	GATGGCAAGATCTGTACCGTGACGGGCTGGGGCAACACGAGTACTATGGCCAACAGGCC	1163
Sbjct	1015	GATGGCAAGATCTGCACGGTGACTGGCTGGGGCAACACGAGTACTACGGCCAACAGGCT	1074
Query	1164	GGGGTACTCCAGGAGGCTCGAGTCCCCATAATCAGCAATGATGTCTGCAATGGCGCTGAC	1223
Sbjct	1075	GGGGTGCTCCAGGAGGCCCGAGTCCCCATAATCAGCAATGATGTCTGCAACGGCCCGAC	1134
Query	1224	TTCTATGGAAACAGATCAAGCCCAAGATGTTCTGTGCTGGCTACCCGAGGGTGGCATT	1283
Sbjct	1135	TTCTACGGGAACAGATCAAGCCCAAGATGTTCTGTGCTGGCTACCCGAGGGTGGCATT	1194
Query	1284	GATGCCTGCCAGGGCGACAGCGGTGGTCCCTTTGTGTGTGAGGACAGCATCTCTCGGACG	1343
Sbjct	1195	GATGCCTGCCAGGGCGACAGTGGTGGCCCTTCGTGTGTGAGGATAGCATCTCTCGGACG	1254

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Query 1344 CCACGTTGGCGGCTGTGTGGCATTGTGAGTTGGGGCACTGGCTGTGCCCTGGCCCAGAAG 1403
Sbjct 1255 CCACGTTGGCGGCTGTGTGGCATTGTGAGCTGGGGCACC GGCTGTGCCCTGGCCCAGAAG 1314

Query 1404 CCAGGCGTCTACACCAAAGTCAGTGACTTCCGGGAGTGGATCTTCCAGGCCATAAAGACT 1463
Sbjct 1315 CCAGGCGTCTACACCAAAGTCAGTGACTTCCGGGAGTGGATCTTCCAGGCCATAAAGACT 1374

Query 1464 CACTCCGAAGCCAGCGGCATGGTGACCCAGCTCTGACCGGTGGCTTCTC---GCTGCGCA 1520
Sbjct 1375 CACTCCGAAGCCAGCGGCATGGTAACCCAGCTTTGACCTGTGGCTTCTCCTCGCTGTGCA 1434

Query 1521 -GCCTCCAGGGCCCGAGGTGATC-----CC---G-----GTGGTGGGATCCACGCTG 1563
Sbjct 1435 CGCCTCCAGGGCCCGAGGTGATCTAAGGGGCCCCAGCCCCACGTGATGGGGTTACCCCTG 1494


Query 1564 GGCCGAGG-ATGGGACGTTTTTCTTCTTGGGCCCGGTCCACAGGTCCAAGGACACCCT-C 1621
Sbjct 1495 GGCC-AGGGATGGAACATTTTTCTTCTTGGGCCCAGCCACAGGTCCAAGGATACTCTTC 1553

Query 1622 CCTCCAGGTCCTCTCTTCCACAGTGGCGGGCCCACTCAGCCCCGAGACCACCCAACTC 1681
Sbjct 1554 CCTCCAAGGTCCTC-C---ACAGTGGCGGGCCCACTCAGCCCTGGGACCACCC---TC 1604

Query 1682 ACCCTCCTGACCCCCATGTAAATATTGTTCTGCTGTCTGGGACTCCTG-----TCTAGGT 1736
Sbjct 1605 -C--TGC---CCCCATGTAAATATTGTTCTGCCATCTGGGACCCCCCCCCCATCTTG-T 1657

Query 1737 GCCCTGATGATGGGATGCTCTTTAAATAATAAAGATGGTTTTGATT 1783
Sbjct 1658 GTCCTGAAGACAGGATGCTCTTTAAATAATAAAGATGGTTTTGATT 1704

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>ref|XM_541697.2|  PREDICTED: Canis familiaris similar to Serine protease hepsin (Transmembrane protease, serine 1) (LOC484583), mRNA
Length=1460

GENE ID: 484583 HPN | hepsin (transmembrane protease, serine 1)
[Canis lupus familiaris]

Score = 1873 bits (1014), Expect = 0.0
Identities = 1322/1470 (89%), Gaps = 24/1470 (1%)
Strand=Plus/Plus

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Query 75 CGCCTCTGCCTCCAGGCCGCCCGCTGCTGCGGGGCCACCATGCTCCTGCCAGGCCTGGA 134
Sbjct 1 CGCCTCTGCCTCCGGGCC-ACCGC--C-GCGGGGCCACCATGCTCCCGCCAGGCCTGGA 56

Query 135 GACTGACCC-GACCCCGGCACTACCTCGAGGCTCCGCCCCACCTGCTGGACCCAGGGT 193
Sbjct 57 GACTGACCCGGA-GAGGGCACTATCTC-A-GCTCCGCCCCACCTGCCGGACCCAGGGT 113

Query 194 CCCACCTGGCCCAAGGAGGTGAGCCAGGGAATCATTAAACAAGAGGCAGTGACATGGCGCA 253
Sbjct 114 CCCACCCCGGCCCGGAGGTGAGCCGGGGAATCATTAAACAAGAGGCCGTGACATGGCGGA 173

Query 254 GAAGGAGGGTGGCCGACTGTGCCATGCTGCTCCAGACCCAAGGTGGCAGCTCTCACTGC 313
Sbjct 174 GAAGGAGGGTGGCCGACTGTGCCATGCTGTTCCGGAACCAAGGTGGCAGCTCTCACTGC 233

Query 314 GGGGACCTGCTACTTCTGACAGCCATCGGGCGGCATCCTGGGCCATTGTG-GCTGTTC 372
Sbjct 234 AGGGACCTGCTGCTCCTGACAGGCATCGGGCGAGCGTCTGGGCCATTGTGACCT-TCC 292

Query 373 TCCTCAGGAGTGACAGGAGCCGCTGTACCCAGTGACAGGTGAGCTCTGCGGAC-GCTCGG 431
Sbjct 293 TACTCAAGAGTGATCAGGAGCCGCTGTATCCGGTGACAGGCCAGCCCTGCCGACGGC-CGG 351

Query 432 CTCATGGTCTTTGACAAGACGGAAGGG-ACGTGGCGGCTGCTGTGCTCCTCGCGCTCCAA 490
Sbjct 352 CTCATGGTGTTCGACGACACGG-AGGGCAGTGGCGGCTGCTGTGCTCCTCGCGCTCCAA 410

Query 491 CGCCAGGGTAGCCGGACTCAGTGCAGGAGATGGGCTTCCTCAGGGCACTGACCCACTC 550
Sbjct 411 CGCCAGGGTGGCGGCCCTGAGCTGCGAGGAGATGGGCTTCCTCAGGGCCCTGGGCCACTC 470

Query 551 CGAGCTGGACGTGCGAACGGCGGGCGCCAATGGCACGTCGGGCTTCTTCTGTGTGGACGA 610
Sbjct 471 GGAGCTGGACGTGCGGACGGCGGGCGCCAACGGCACGTCGGGCTTCTTCTGCGTGGACGA 530

Query 611 GGGGAGGCTGCCCCACACCCAGAGGTGCTGGAGGTGATCTCCGTGTGTGATTGCCCCAG 670
Sbjct 531 GGGGAGGCTGCCCTGGCCCGAGGCTGCTCGAGGTGATCTCCGTGTGTGACTGTCCCAG 590

Query 671 AGGCCGTTTCTTGGCCGCCATCTGCCAAGACTGTGGCCGAGGAAGCTGCCCGTGGACCG 730
Sbjct 591 GGGCCGTTTCTTGGCTACCGTCTGCCAAGATTGTGGCCGAAGGAAGCTGCCTGTGGATCG 650

Query 731 CATCGTGGGAGGCCGGACACAGCTTGGGCCGGTGGCCGTGGCAAGTCAGCCTTCGCTA 790
Sbjct 651 CATCGTTGGAGGCCAAGACACAGCCTGGGCAGGTGGCCGTGGCAAGTCAGTCTTCGCTA 710

Query 791 TGATGGAGCACACCTCTGTGG-GGGATCCCTGCTCTCCGGGACTGGGTGCTGACAGCCG 849
Sbjct 711 CGATGGAGCACACCTCTGTGGAGGG-TCCCTGCTGTGAGGAGACTGGGTGCTGACAGCCG 769


Query 850 CCCACTGCTTCCCGAGCGGAACCGGGTCTGTCCCGATGGCGAGTGTGTCGGGTGCCG 909

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Sbjct  770  CCCACTGCTTCCCCGAGCGGAACCGGGTCCTGTCTCGGTGGCGAGTGTTCGCCGCGCCG  829
Query   910  TGGCCCAGGCCTCTCCCCACGGTCTGCAGCTGGGGGTGCAGGCTGTGGTCTACCACGGGG  969
Sbjct  830  TGGCCCAGGCCTCACCCCATGGCCTGCAGCTGGGGGTGCAGGCAGTAGTCTACCACGGGG  889
Query   970  GCTATCTTCCCTTTTCGGGACCCCAACAGCGAGGAGAACAGCAACGATATTGCCCTGGTCC  1029
Sbjct  890  GCTACCTCCCCCTTCGAGACCCCAACAGTGAGGAAAACAGCAATGACATTGCCCTGGTCC  949
Query  1030  ACCTCTCCAGTCCCCTGCCCTCACAGAATACATCCAGCCTGTGTGCCTCCCAGCTGCCG  1089
Sbjct  950  ACCTGTCCAGCCCCCTGCCCTCACAGAGTACATCCAGCCCCTGTGCCTCCCGGCGGCCG  1009
Query  1090  GCCAGGCCCTGGTGGATGGCAAGATCTGTACCGTGACGGGCTGGGGCAACACGCAGTACT  1149
Sbjct  1010  GCCAGGCCCTGGTGGACGGCAAGATCTGCACGGTGACCGGCTGGGGCAACACGCAGTACT  1069
Query  1150  ATGGCCAAACAGGCCGGGGTACTCCAGGAGGCTCGAGTCCCCATAATCAGCAATGATG-TC  1208
Sbjct  1070  ACGGCCAACAGGCTGGGGTGCTCCAGGAGGCCCGAGTCCCCATCATCAGCAACGA-GCTG  1128
Query  1209  TGCAATGGCGCTGACTTCTATG-GAAACCAGATCAAGCCCAAGATGTTCTGTGCTGGCTA  1267
Sbjct  1129  TGCACGGCCCCGACTTCTACGCGAA-CCAGATCAAGCCCAAGATGTTCTGTGCCGGCTA  1187
Query  1268  CCCCAGAGGTGGCATTGATGCCTGCCAGGGCGACAGCGGTGGTCCCTTGTGTGTGAGGA  1327
Sbjct  1188  CCCCAGAGGGCGGCATCGATGCCTGCCAGGGCGACAGCGGCGGCCCTTCGTGTGTGAGGA  1247
Query  1328  CAGCATCTCTCGGACGCCACGTTGGCGGCTGTGTGGCATGTGAGTTGGGGCACTGGCTG  1387
Sbjct  1248  CAGCATCTCTCGGACGCCACGTTGGCGGCTGTGTGGCATCGTGAGCTGGGGCACCGGCTG  1307
Query  1388  TGCCCTGGCCCAGAAGCCAGGCGTCTACACCAAAGTCAGTGACTTCCGGGAGTGGATCTT  1447
Sbjct  1308  TGCCCTGGCCCAGAAGCCAGGTGTCTACACCAAAGTCAGTGACTTCCGGGAGTGGATCTT  1367
Query  1448  CCAGGCCATAAAGACTCACTCCGAAGCCAGCGGCATGGTGACCCAGCTCTGACCGGTGGC  1507
Sbjct  1368  CCAGGCCATAAAGACTCACTCCGAAGCCAGCGGCATGGTGACCCAGCTCTGACCTGTGGC  1427
Query  1508  TTCTC---GCTGCGCA-GCCTCCAGGGCCC  1533
Sbjct  1428  TTGTCCTTGATGCGCACGCCTCCAGGGCCC  1457

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>ref|XM_001157575.1|  PREDICTED: Pan troglodytes hepsin (transmembrane protease, serine 1), transcript variant 2 (HPN), mRNA
Length=1695

GENE ID: 455944 HPN | hepsin (transmembrane protease, serine 1)
[Pan troglodytes]

Sort alignments for this subject sequence by:
E value Score Percent identity
Query start position Subject start position

Score = 1868 bits (1011), Expect = 0.0
Identities = 1015/1017 (99%), Gaps = 0/1017 (0%)
Strand=Plus/Plus

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Query   191  GGTCCCACCTTGGCCAGGAGGTACGCCAGGGAATCATTAAACAAGAGGCAGTGACATGGC  250
Sbjct  146  GGTCCCACCTTGGCCAGGAGGTACGCCAGGGAATCATTAAACAAGAGGCAGTGACATGGC  205
Query   251  GCAGAAGGAGGGTGGCCGGAAGTGTGCCATGCTGTCCAGACCCAAGGTGGCAGCTCTCAC  310
Sbjct  206  GCAGAAGGAGGGTGGCCGGAAGTGTGCCATGCTGTCCAGACCCAAGGTGGCAGCTCTCAC  265
Query   311  TGCGGGGACCTTGCTACTTCTGACAGCCATCGGGGCGGCATCCTGGGCCATTGTGGCTGT  370
Sbjct  266  TGCGGGGACCTTGCTACTTCTGACAGCCATCGGGGCGGCATCCTGGGCCATTGTGGCTGT  325
Query   371  TCTCCTCAGGAGTGACAGGAGCCGCTGTACCCAGTGACAGGTAGCTCTGCGGACGCTCG  430
Sbjct  326  TCTCCTCAGGAGTGACAGGAGCCGCTGTACCCAGTGACAGGTAGCTCTGCGGACGCTCG  385
Query   431  GCTCATGGTCTTTGACAAGACGGAAGGGACGTGGCGGCTGCTGTGCTCCTCGCGCTCCAA  490
Sbjct  386  GCTCATGGTCTTTGACAAGACGGAAGGGACGTGGCGGCTGCTGTGCTCCTCGCGCTCCAA  445
Query   491  CGCCAGGGTAGCCGGAAGTCACTGCGAGGAGATGGGCTTCCTCAGGGCACTGACCCACTC  550
Sbjct  446  CGCCAGGGTAGCCGGAAGTCACTGCGAGGAGATGGGCTTCCTCAGGGCACTGACCCACTC  505
Query   551  CGAGCTGGACGTGCGAACGGCGGGCGCCAATGGCACGTGGGGCTTCTTCTGTGTGGACGA  610
Sbjct  506  CGAGCTGGACGTGCGAACGGCGGGCGCCAATGGCACGTGGGGCTTCTTCTGTGTGGACGA  565
Query   611  GGGGAGGCTGCCCCACACCCAGAGGCTGCTGGAGGTATCTCCGTGTGTGATTGCCCCAG  670
Sbjct  566  GGGGAGGCTGCCCCACACCCAGAGGCTGCTGGAGGTATCTCCGTGTGTGATTGCCCCAG  625
Query   671  AGGCCGTTTCTTGGCCGCCATCTGCCAAGACTGTGGCCGCGAGGAAGCTGCCCGTGGACCG  730

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Sbjct  626  AGGCCGTTTCTTGGCCGCCATCTGCCAAGACTGTGGCCGACGGAAGCTGCCCCGTGGACCG 685
Query   731  CATCGTGGGAGGCCGGGACACCAGCTTGGGCCGGTGGCCGTGGCAAGTCAGCCTTCGCTA 790
Sbjct  686  CATCGTGGGAGGCCGGGACACCAGCTTGGGCCGGTGGCCGTGGCAAGTCAGCCTTCGCTA 745
Query   791  TGATGGAGCACACCTCTGTGGGGGATCCCTGCTCTCCGGGGACTGGGTGCTGACAGCCGC 850
Sbjct  746  TGATGGAGCACACCTCTGTGGGGGATCCCTGCTCTCCGGGGACTGGGTGCTGACAGCCGC 805
Query   851  CCACTGCTTCCCGAGCGGAACCGGGTCCTGTCCCGATGGCGAGTGTTGCCCGGTGCCGT 910
Sbjct  806  CCACTGCTTCCCGAGCGGAACCGGGTCCTGTCCCGATGGCGAGTGTTGCCCGGTGCCGT 865
Query   911  GGCCCAGGCCTCTCCCCACGGTCTGCAGCTGGGGGTGCAGGCTGTGGTCTACCACGGGGG 970
Sbjct  866  GGCCCAGGCCTCTCCCCACGGCCTGCAGCTGGGGGTGCAGGCTGTGGTCTACCACGGGGG 925
Query   971  CTATCTTCCCTTTCGGGACCCCAACAGCGAGGAGAACAGCAACGATATTGCCCTTGGTCCA 1030
Sbjct  926  CTATCTTCCCTTTCGGGACCCCAACAGCGAGGAGAACAGCAACGATATTGCCCTTGGTCCA 985
Query  1031  CCTCTCCAGTCCCCTGCCCTCACAGAATACATCCAGCCTGTGTGCCTCCCAGCTGCCGG 1090
Sbjct  986  CCTCTCCAGTCCCCTGCCCTCACAGAATACATCCAGCCTGTGTGCCTCCCAGCTGCCGG 1045
Query  1091  CCAGGCCCTGGTGGATGGCAAGATCTGTACCGTGACGGGCTGGGGCAACACGCAGTACTA 1150
Sbjct  1046  CCAGGCCCTGGTGGATGGCAAGATCTGTACCGTGACGGGCTGGGGCAACACGCAGTACTA 1105
Query  1151  TGGCCAACAGGCCGGGGTACTCCAGGAGGCTCGAGTCCCCATAATCAGCAATGATGT 1207
Sbjct  1106  TGGCCAACAGGCCGGGGTACTCCAGGAGGCTCGAGTCCCCATAATCAGCAATGATGT 1162


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Score = 968 bits (524), Expect = 0.0
 Identities = 528/530 (99%), Gaps = 0/530 (0%)
 Strand=Plus/Plus

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Query  1254  TTCTGTGTGGCTACCCCGAGGGTGGCATTGATGCCTGCCAGGGCGACAGCGGTGGTCCC 1313
Sbjct  1164  TTCTGTGTGGCTACCCCGAGGGTGGCATTGATGCCTGCCAGGGCGACAGCGGTGGTCCC 1223
Query  1314  TTTGTGTGTGAGGACAGCATCTCTCGGACGCCACGTTGGCGGCTGTGTGGCATTGTGAGT 1373
Sbjct  1224  TTTGTGTGTGAGGACAGCATCTCTCGGACGCCACGTTGGCGGCTGTGTGGCATTGTGAGT 1283
Query  1374  TGGGGCACTGGCTGTGCCTGGCCCAGAAGCCAGGCGTCTACACCAAAGTCAGTGACTTC 1433
Sbjct  1284  TGGGGCACTGGCTGTGCCTGGCCCAGAAGCCAGGCGTCTACACCAAAGTCAGTGACTTC 1343
Query  1434  CGGGAGTGGATCTTCCAGGCCATAAAGACTCACTCCGAAGCCAGCGGCATGGTGACCCAG 1493
Sbjct  1344  CGGGAGTGGATCTTCCAGGCCATAAAGACTCACTCCGAAGCCAGCGGCATGGTGACCCAG 1403
Query  1494  CTCTGACCGGTGGCTTCTCGCTGCGCAGCCTCCAGGGCCCGAGGTGATCCCGGTGGTGGG 1553
Sbjct  1404  CTCTGACCGGTGGCTTCTCGCTGCGCAGCCTCCAGGGCCCGAGGTGATCCCGGTGGTGGG 1463
Query  1554  ATCCACGCTGGGCCGAGGATGGGACGTTTTTCTTCTTGGGCCCGGTCCACAGGTCCAAGG 1613
Sbjct  1464  ATCCACGCTGGGCCCTAGGATGGGACGTTTTTCTTCTTGGGCCCGGTCCACAGGTCCAAGG 1523
Query  1614  ACACCCCTCCCTCCAGGGTCCTCTCTTCCAAGTGGCGGGGCCACTCAGCCCCGAGACCAC 1673
Sbjct  1524  ACACCCCTCCCTCCAGGGTCCTCTCTTCCAAGTGGCGGGGCCACTCAGCCCCGAGACCAC 1583
Query  1674  CCAACCTCACCTCCTGACCCCATGTAAATATTGTTCTGCTGTCTGGGACTCCTGTCTA 1733
Sbjct  1584  CCAACCTCACCTCCTGACCCCATGTAAATATTGTTCTGCTGTCTGGGACTCCTGTCTA 1643
Query  1734  GGTGCCCTGATGATGGGATGCTCTTTAAATAATAAAGATGGTTTTGATT 1783
Sbjct  1644  GGTGCCCTGATGACGGGATGCTCTTTAAATAATAAAGATGGTTTTGATT 1693

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>emb|CR597177.1|  full-length cDNA clone CS0DJ003YL08 of T cells (Jurkat cell line)
 Cot 10-normalized of Homo sapiens (human)
 Length=1828

GENE ID: 3249 HPN | hepsin (transmembrane protease, serine 1) [Homo sapiens]
 (Over 10 PubMed links)

Sort alignments for this subject sequence by:
 E value Score Percent identity
 Query start position Subject start position

Score = 1714 bits (928), Expect = 0.0
 Identities = 928/928 (100%), Gaps = 0/928 (0%)
 Strand=Plus/Plus

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Query  533  CAGGGCACTGACCCACTCCGAGCTGGACGTGCGAACGGCGGGCGCCAATGGCACGTCGGG 592
Sbjct  375  CAGGGCACTGACCCACTCCGAGCTGGACGTGCGAACGGCGGGCGCCAATGGCACGTCGGG 434
Query  593  CTTCTTCTGTGTGGACGAGGGGAGGCTGCCCCACACCCAGAGGCTGCTGGAGGTCACTTC 652

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Sbjct  435  CTTCTTCTGTGTGGACGAGGGGAGGCTGCCCCACACCCAGAGGCTGCTGGAGGTCATCTC 494
Query  653  CGTGTGTGATTGCCCCAGAGGCCGTTTCTTGGCCGCCATCTGCCAAGACTGTGGCCGCAG 712
      |||
Sbjct  495  CGTGTGTGATTGCCCCAGAGGCCGTTTCTTGGCCGCCATCTGCCAAGACTGTGGCCGCAG 554
Query  713  GAAGCTGCCCCGTGGACCGCATCGTGGGAGGCCGGGACACCAGCTTGGGCCGGTGGCCGTG 772
      |||
Sbjct  555  GAAGCTGCCCCGTGGACCGCATCGTGGGAGGCCGGGACACCAGCTTGGGCCGGTGGCCGTG 614
Query  773  GCAAGTCAGCCTTCGCTATGATGGAGCACACCTCTGTGGGGGATCCCTGCTCTCCGGGGA 832
      |||
Sbjct  615  GCAAGTCAGCCTTCGCTATGATGGAGCACACCTCTGTGGGGGATCCCTGCTCTCCGGGGA 674
Query  833  CTGGGTGCTGACAGCCGCCCACTGCTTCCCGGAGCGGAACCGGGTCCTGTCCCGATGGCG 892
      |||
Sbjct  675  CTGGGTGCTGACAGCCGCCCACTGCTTCCCGGAGCGGAACCGGGTCCTGTCCCGATGGCG 734
Query  893  AGTGTTTGCCCGGTGCCGTGGCCCGAGGCCTCTCCCCACGGTCTGCAGCTGGGGGTGCAGGC 952
      |||
Sbjct  735  AGTGTTTGCCCGGTGCCGTGGCCCGAGGCCTCTCCCCACGGTCTGCAGCTGGGGGTGCAGGC 794
Query  953  TGTGGTCTACCACGGGGGCTATCTTCCCTTTCGGGACCCCAACAGCGAGGAGAACAGCAA 1012
      |||
Sbjct  795  TGTGGTCTACCACGGGGGCTATCTTCCCTTTCGGGACCCCAACAGCGAGGAGAACAGCAA 854
Query  1013 CGATATTGCCCTGGTCCACCTCTCCAGTCCCCTGCCCTCACAGAATACATCCAGCCTGT 1072
      |||
Sbjct  855  CGATATTGCCCTGGTCCACCTCTCCAGTCCCCTGCCCTCACAGAATACATCCAGCCTGT 914
Query  1073 GTGCCTCCCAGCTGCCGGCCAGGCCCTGGTGGATGGCAAGATCTGTACCGTGACGGGCTG 1132
      |||
Sbjct  915  GTGCCTCCCAGCTGCCGGCCAGGCCCTGGTGGATGGCAAGATCTGTACCGTGACGGGCTG 974
Query  1133 GGGCAACACGCAGTACTATGGCCAAACAGGCCGGGGTACTCCAGGAGGCTCGAGTCCCCAT 1192
      |||
Sbjct  975  GGGCAACACGCAGTACTATGGCCAAACAGGCCGGGGTACTCCAGGAGGCTCGAGTCCCCAT 1034
Query  1193 AATCAGCAATGATGTCTGCAATGGCGCTGACTTCTATGGAAACCAGATCAAGCCCAAGAT 1252
      |||
Sbjct  1035 AATCAGCAATGATGTCTGCAATGGCGCTGACTTCTATGGAAACCAGATCAAGCCCAAGAT 1094
Query  1253 GTTCTGTGCTGGCTACCCGAGGGTGGCATTGATGCCTGCCAGGGCGACAGCGGTGGTCC 1312
      |||
Sbjct  1095 GTTCTGTGCTGGCTACCCGAGGGTGGCATTGATGCCTGCCAGGGCGACAGCGGTGGTCC 1154
Query  1313 CTTTGTGTGTGAGGACAGCATCTCTCGGACGCCACGTTGGCGCTGTGTGGCATTGTGAG 1372
      |||
Sbjct  1155 CTTTGTGTGTGAGGACAGCATCTCTCGGACGCCACGTTGGCGCTGTGTGGCATTGTGAG 1214
Query  1373 TTGGGGCACTGGCTGTGCCCTGGCCAGAGCCAGGCGTCTACACCAAAGTCAGTGACTT 1432
      |||
Sbjct  1215 TTGGGGCACTGGCTGTGCCCTGGCCAGAGCCAGGCGTCTACACCAAAGTCAGTGACTT 1274
Query  1433 CCGGGAGTGGATCTTCCAGGCCATAAAG 1460
      |||
Sbjct  1275 CCGGGAGTGGATCTTCCAGGCCATAAAG 1302

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Score = 566 bits (306), Expect = 1e-157
 Identities = 310/312 (99%), Gaps = 0/312 (0%)
 Strand=Plus/Plus

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Query  1459 AGACTCACTCCGAAGCCAGCGGCATGGTGACCCAGCTCTGACCGGTGGCTTCTCGCTGCG 1518
      |||
Sbjct  1517 AGACTCACTCCGAAGCCAGCGGCATGGTGACCCAGCTCTGACCGGTGGCTTCTCGCTGCG 1576
Query  1519 CAGCCTCCAGGGCCCGAGGTGATCCCGGTGGTGGGATCCACGCTGGGCCGAGGATGGGAC 1578
      |||
Sbjct  1577 CAGCCTCCAGGGCCCGAGGTGATCCCGGTGGTGGGATCCACGCTGGGCCGAGGATGGGAC 1636
Query  1579 GTTTTTCTTCTTGGGCCCGGTCCACAGGTCCAAGGACACCCCTCCCTCCAGGGTCCTCTCT 1638
      |||
Sbjct  1637 GTTTTTCTTCTTGGGCCCGGTCCACAGGTCCAAGGACACCCCTCCCTCCAGGGTCCTCTCT 1696
Query  1639 TCCACAGTGGCGGGCCCACTCAGCCCGGAGACCACCAACCTCACCTCCTGACCCCCAT 1698
      |||
Sbjct  1697 TCCACAGTGGCGGGCCCACTCAGCCCGGAGACCACCAACCTCACCTCCTGACCCCCAT 1756
Query  1699 GTAAATATTGTTCTGCTGTCTGGGACTCCTGTCTAGGTGCCCCGATGATGGGATGCTCT 1758
      |||
Sbjct  1757 GTAAATATTGTTCTGCTGTCTGGGACTCCTGTCTAGGTGCCCCGATGACGGGATGCTCT 1816
Query  1759 TTAAATAATAAA 1770
      |||
Sbjct  1817 TTAAATAATAAA 1828

```

Score = 326 bits (176), Expect = 3e-85
 Identities = 176/176 (100%), Gaps = 0/176 (0%)
 Strand=Plus/Plus

```

Query  86  CCAGGCCGCCCGCTGCTGCGGGGCCACCATGCTCCTGCCAGGCCTGGAGACTGACCCGA 145
      |||
Sbjct  1  CCAGGCCGCCCGCTGCTGCGGGGCCACCATGCTCCTGCCAGGCCTGGAGACTGACCCGA 60
Query  146  CCCCCGCACTACCTCGAGGCTCCGCCCCCACTGTGGACCCCAAGGTCCCACCTGGCC 205
      |||

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Sbjct  61  CCCCCGCACTACCTCGAGGCTCCGCCCCACCTGCTGGACCCCAGGGTCCCACCCTGGCC 120
Query  206  CAGGAGGTCAGCCAGGGAATCATTAACAAGAGGCAGTGACATGGCGCAGAAGGAGG 261
      |||||
Sbjct  121  CAGGAGGTCAGCCAGGGAATCATTAACAAGAGGCAGTGACATGGCGCAGAAGGAGG 176


Score = 244 bits (132), Expect = 8e-61
Identities = 132/132 (100%), Gaps = 0/132 (0%)
Strand=Plus/Plus

Query  405  GTGCAGGTCAGCTCTGCGGACGCTCGGCTCATGGTCTTTGACAAGACGGAAGGGACGTGG 464
Sbjct  176  GTGCAGGTCAGCTCTGCGGACGCTCGGCTCATGGTCTTTGACAAGACGGAAGGGACGTGG 235

Query  465  CGGCTGCTGTGCTCCTCGCGCTCCAACGCCAGGGTAGCCGGA CTGAGCTGCGAGGAGATG 524
Sbjct  236  CGGCTGCTGTGCTCCTCGCGCTCCAACGCCAGGGTAGCCGGA CTGAGCTGCGAGGAGATG 295

Query  525  GGCTTCCTCAGG 536
Sbjct  296  GGCTTCCTCAGG 307

```

>emb|CR592189.1|  full-length cDNA clone CS0DM012Y015 of Fetal liver of Homo sapiens (human)
Length=1212

GENE ID: 3249 HPN | hepsin (transmembrane protease, serine 1) [Homo sapiens]
(Over 10 PubMed links)

Sort alignments for this subject sequence by:
E value Score Percent identity
Query start position Subject start position

```

Score = 1663 bits (900), Expect = 0.0
Identities = 911/916 (99%), Gaps = 2/916 (0%)
Strand=Plus/Plus

Query  856  GCTTCC-CGGAGCGGAACCGGGTCCTGTCCCGATGGCGAGTGTTTGCCGGTGCCGTGGCC 914
      |||||
Sbjct  298  GCTTCTCTAG-GCGGAACCGGGTCCTGTCCCGATGGCGAGTGTTTGCCGGTGCCGTGGCC 356

Query  915  CAGGCCTCTCCCCACGGTCTGCAGCTGGGGGTGCAGGCTGTGGTCTACACGGGGGCTAT 974
Sbjct  357  CAGGCCTCTCCCCACGGTCTGCAGCTGGGGGTGCAGGCTGTGGTCTACACGGGGGCTAT 416

Query  975  CTTCCCTTTTCGGGACCCCAACAGCGAGGAGAACAGCAACGATATTGCCCTGGTCCACCTC 1034
Sbjct  417  CTTCCCTTTTCGGGACCCCAACAGCGAGGAGAACAGCAACGATATTGCCCTGGTCCACCTC 476

Query  1035  TCCAGTCCCCTGCCCCCTCACAGAATACATCCAGCCTGTGTGCCTCCCAGCTGCCGGCCAG 1094
Sbjct  477  TCCAGTCCCCTGCCCCCTCACAGAATACATCCAGCCTGTGTGCCTCCCAGCTGCCGGCCAG 536

Query  1095  GCCCTGGTGGATGGCAAGATCTGTACCGTGACGGGCTGGGGCAACACGCAGTACTATGGC 1154
Sbjct  537  GCCCTGGTGGATGGCAAGATCTGTACCGTGACGGGCTGGGGCAACACGCAGTACTATGGC 596

Query  1155  CAACAGGCCGGGGTACTCCAGGAGGCTCGAGTCCCCATAATCAGCAATGATGTCTGCAAT 1214
Sbjct  597  CAACAGGCCGGGGTACTCCAGGAGGCTCGAGTCCCCATAATCAGCAATGATGTCTGCAAT 656

Query  1215  GGCCTGACTTCTATGGAACAGATCAAGCCCAAGATGTTCTGTGCTGGCTACCCCGAG 1274
Sbjct  657  GGCCTGACTTCTATGGAACAGATCAAGCCCAAGATGTTCTGTGCTGGCTACCCCGAG 716

Query  1275  GGTGGCATTGATGCCTGCCAGGGCGACAGCGGTGGTCCCTTTGTGTGTGAGGACAGCATC 1334
Sbjct  717  GGTGGCATTGATGCCTGCCAGGGCGACAGCGGTGGTCCCTTTGTGTGTGAGGACAGCATC 776

Query  1335  TCTCGGACGCCACGTTGGCGGCTGTGTGGCATTGTGAGTTGGGGCACTGGCTGTGCCCTG 1394
Sbjct  777  TCTCGGACGCCACGTTGGCGGCTGTGTGGCATTGTGAGTTGGGGCACTGGCTGTGCCCTG 836

Query  1395  GCCCAGAAGCCAGGCGTCTACACCAAAGTCAGTGACTTCCGGGAGTGGATCTTCCAGGCC 1454
Sbjct  837  GCCCAGAAGCCAGGCGTCTACACCAAAGTCAGTGACTTCCGGGAGTGGATCTTCCAGGCC 896

Query  1455  ATAAAGACTCACTCCGAAGCCAGCGGCATGGTGACCCAGCTCTGACCGGTGGCTTCTCGC 1514
Sbjct  897  ATAAAGACTCACTCCGAAGCCAGCGGCATGGTGACCCAGCTCTGACCGGTGGCTTCTCGC 956

Query  1515  TGCGCAGCCTCCAGGGCCCAGGTGATCCCGGTGGTGGGATCCACGCTGGGCGGAGGATG 1574
Sbjct  957  TGCGCAGCCTCCAGGGCCCAGGTGATCCCGGTGGTGGGATCCACGCTGGGCGGAGGATG 1016

Query  1575  GGACGTTTTTCTTCTTGGGCCCGGTCCACAGGTCCAAGGACACCCTCCCTCCAGGGTCCT 1634
Sbjct  1017  GGACGTTTTTCTTCTTGGGCCCGGTCCACAGGTCCAAGGACACCCTCCCTCCAGGGTCCT 1076

Query  1635  CTCTTCCACAGTGGCGGGCCCACTCAGCCCCGAGACCACCCAACCTCACCTCCTGACCC 1694
Sbjct  1077  CTCTTCCACAGTGGCGGGCCCACTCAGCCCCGAGACCACCCAACCTCACCTCCTGACCC 1136

Query  1695  CCATGTAAATATTGTTCTGTCTGGGACTCCTGTCTAGGTGCCCTGATGATGGGATG 1754
      |||||

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Sbjct  1137  CCATGTAAATATGTTCTGCTGCTCTGGGACTCCTGTCTAGGTGCCCCGTGATGACGGGATG  1196
Query   1755  CTCTTTAAATAATAAA  1770
          |||
Sbjct  1197  CTCTTTAAATAATAAA  1212

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Score = 327 bits (177), Expect = 8e-86
 Identities = 177/177 (100%), Gaps = 0/177 (0%)
 Strand=Plus/Plus

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Query   85  TCCAGGCCGCCCCGCTGCTGCGGGGCCACCATGCTCCTGCCCAGGCCTGGAGACTGACCCG  144
Sbjct   1  TCCAGGCCGCCCCGCTGCTGCGGGGCCACCATGCTCCTGCCCAGGCCTGGAGACTGACCCG  60
Query  145  ACCCCGGCACTACCTCGAGGCTCCGCCCCACCTGTGGACCCAGGGTCCCACCTGGC  204
Sbjct  61  ACCCCGGCACTACCTCGAGGCTCCGCCCCACCTGTGGACCCAGGGTCCCACCTGGC  120
Query  205  CCAGGAGGTCAGCCAGGGAATCATTAACAAGAGGCAGTGACATGGCGCAGAAGGAGG  261
Sbjct  121  CCAGGAGGTCAGCCAGGGAATCATTAACAAGAGGCAGTGACATGGCGCAGAAGGAGG  177

```

Score = 244 bits (132), Expect = 8e-61
 Identities = 132/132 (100%), Gaps = 0/132 (0%)
 Strand=Plus/Plus

```

Query  405  GTGCAGGTGAGCTCTGCGGACGCTCGGCTCATGGTCTTTGACAAGACGGAAGGGACGTGG  464
Sbjct  177  GTGCAGGTGAGCTCTGCGGACGCTCGGCTCATGGTCTTTGACAAGACGGAAGGGACGTGG  236
Query  465  CGGCTGCTGTGCTCCTCGCGCTCCACGCCAGGGTAGCCGGACTCAGCTGCGAGGAGATG  524
Sbjct  237  CGGCTGCTGTGCTCCTCGCGCTCCACGCCAGGGTAGCCGGACTCAGCTGCGAGGAGATG  296
Query  525  GGCTTCCTCAGG  536
Sbjct  297  GGCTTCCTCAGG  308

```

>emb|CU693029.1| Synthetic construct Homo sapiens gateway clone IMAGE:100019300
 3' read HPN mRNA
 Length=1184

Score = 1653 bits (895), Expect = 0.0
 Identities = 1070/1151 (92%), Gaps = 26/1151 (2%)
 Strand=Plus/Minus

```


Query  355  GGGC-CATTGTGGCTGTTCTCCTCAGGAGTGAC-CAGGAGCCGCTG-TACCCAGTGCAGG  411
Sbjct  1148  GGGCACATGGTGGGT-TTTTCTCGGGAG-GGCACAGGAGCC-CTGTTA-CCAGGGGAGG  1093
Query  412  TCAGCTCTGCGGACG-CTC-GGCTCATGGTCTTTGACAAGACGGAAGGGACGT-GGCGGC  468
Sbjct  1092  TTAACCTTG-GGA-GCCTCGGGTTCA-AGTTTTTGACAAAACGGAAGGGAC-TGGGGGGT  1037
Query  469  TGCTGTGCTCCTCGCGCTCCAACGCCAGGGTAGCCGGACTCAGCTGCGAGGAGATGGGCT  528
Sbjct  1036  TTTTGT-TTCTTG-GGTTCAACCCAGGGAACCCGGA-TTAGCTGCAAGGA-AT-GGCT  982
Query  529  TCCTCAGGGCACTGACCCACTCCGAGCTGGACGTGCGAACGGCGGGCGCAATGGCACGT  588
Sbjct  981  TGCTCAGGGGA-TGACCCGCTCCGAG-GGGACGTGGGGACGGCGGGCGCAATGGCAC-T  925
Query  589  CGGGCTTCTTCTGTGTGGACGAGGGGAGGCTGCCCCACACCCAGAGGCTGCTGGAGGTCA  648
Sbjct  924  TGGGGTTTTTCTG-GGGACGAGGGAAGGCT-CCCCAGACCCAGAGGCGGCTGGAGGTCA  867
Query  649  TCTCCGTGTGTG-ATTGCCCCAGAGGCCGTTTCTTGGCCGCCATCTGCCAAGACTGTGGC  707
Sbjct  866  TCTTCG-GGGGGAATGCCCCAGAGGCCGTTGTTGGCCGCCATCTGCCAAGACTGTGGC  808
Query  708  CGCAGGAAGCTGCCCCGTGGACCGCATCGTGGGAGGCCGGGACACCAGCTTGGGCCGTGG  767
Sbjct  807  CGCAGGAAGCTGCCCCGTGGGCCGCATCGTGGGAGGCCGGGACGCCAGCTTGGGCCGTGG  748
Query  768  CCGTGGCAAGTCAGCCTTCGCTATGATGGAGCACACCTCTGTGGGGATCCCTGCTCTCC  827
Sbjct  747  CGGTGGCAAGTCAGCCTTGGCTATGATGGGGCACACCTCTGTGGGGATCCCTGCTCTCC  688
Query  828  GGGGACTGGGTGCTGACAGCCGCCCACTGCTTCCGGAGCGGAACCGGGTCTGTCCCGA  887
Sbjct  687  GGGGACTGGGTGCTGACAGCCGCCCAATTGCTTCCGGAGCGGAACCGGGTCTGTCCCGA  628
Query  888  TGGCGAGTGTTTTGCCGGTGCCGTGGCCCAGGCCTCTCCCCACGGTCTGCAGCTGGGGGTG  947
Sbjct  627  TGGCGAGTGTTTTGCCGGTGCCGTGGCCCAGGCCTCTCCCCACGGTCTGCAGCTGGGGGTG  568
Query  948  CAGGCTGTGGTCTACCAAGGGGGCTATCTTCCCTTTTCGGGACCCCAACAGCGAGGAGAAC  1007
Sbjct  567  CAGGCTGTGGTCTACCAAGGGGGCTATCTTCCCTTTTCGGGACCCCAACAGCGAGGAGAAC  508
Query  1008  AGCAACGATATTGCCCTGGTCCACCTCTCCAGTCCCCTGCCCTCACAGAATACATCCAG  1067
Sbjct  507  AGCAACGATATTGCCCTGGTCCACCTCTCCAGTCCCCTGCCCTCACAGAATACATCCAG  448
Query  1068  CCTGTGTGCCTCCAGCTGCCGGCCAGGCCTGGTGGATGGCAAGATCTGTACCGTGACG  1127

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```

Sbjct  447  CCTGTGTGCCTCCACAGCTGCCGCCAGGCCCTGGTGGATGGCAAGATCTGTACCGTGACG  388
Query  1128  GGCTGGGGCAACACGCAGTACTATGGCCAACAGGCCGGGGTACTCCAGGAGGCTCGAGTC  1187
Sbjct  387  GGCTGGGGCAACACGCAGTACTATGGCCAACAGGCCGGGGTACTCCAGGAGGCTCGAGTC  328
Query  1188  CCCATAATCAGCAATGATGTCTGCAATGGCGCTGACTTCTATGGAACCAGATCAAGCCC  1247
Sbjct  327  CCCATAATCAGCAATGATGTCTGCAATGGCGCTGACTTCTATGGAACCAGATCAAGCCC  268
Query  1248  AAGATGTTCTGTGCTGGCTACCCCGAGGGTGGCATTGATGCCTGCCAGGGCGACAGCGGT  1307
Sbjct  267  AAGATGTTCTGTGCTGGCTACCCCGAGGGTGGCATTGATGCCTGCCAGGGCGACAGCGGT  208
Query  1308  GGTCCCTTTGTGTGTGAGGACAGCATCTCTCGGACGCCACGTTGGCGGCTGTGTGGCATT  1367
Sbjct  207  GGTCCCTTTGTGTGTGAGGACAGCATCTCTCGGACGCCACGTTGGCGGCTGTGTGGCATT  148
Query  1368  GTGAGTTGGGGCACTGGCTGTGCCCTGGCCCAGAAGCCAGGCGTCTACACCAAAGTCAGT  1427
Sbjct  147  GTGAGTTGGGGCACTGGCTGTGCCCTGGCCCAGAAGCCAGGCGTCTACACCAAAGTCAGT  88
Query  1428  GACTTCCGGGAGTGGATCTTCCAGGCCATAAAGACTCACTCCGAAGCCAGCGGCATGGTG  1487
Sbjct  87  GACTTCCGGGAGTGGATCTTCCAGGCCATAAAGACTCACTCCGAAGCCAGCGGCATGGTG  28
Query  1488  ACCCAGCTCTG  1498
Sbjct  27  ACCCAGCTCTG  17

```

>ref|XM_001157514.1|  PREDICTED: Pan troglodytes hepsin (transmembrane protease, serine 1), transcript variant 1 (HPN), mRNA
Length=2104

GENE ID: 455944 HPN | hepsin (transmembrane protease, serine 1)
[Pan troglodytes]

Sort alignments for this subject sequence by:
E value Score Percent identity
Query start position Subject start position

Score = 1476 bits (799), Expect = 0.0
Identities = 803/805 (99%), Gaps = 0/805 (0%)
Strand=Plus/Plus

```

Query  403  CAGTGCAGGTACAGCTCTGCGGACGCTCGGCTCATGGTCTTTGACAAGACGGAAGGGACGT  462
Sbjct  767  CAGTGCAGGTACAGCTCTGCGGACGCTCGGCTCATGGTCTTTGACAAGACGGAAGGGACGT  826
Query  463  GGCGGCTGCTGTGCTCCTCGCGCTCCAACGCCAGGGTAGCCGACTCAGCTGCGAGGAGA  522
Sbjct  827  GGCGGCTGCTGTGCTCCTCGCGCTCCAACGCCAGGGTAGCCGACTCAGCTGCGAGGAGA  886
Query  523  TGGGCTTCCTCAGGGCACTGACCCACTCCGAGCTGGACGTGCGAACGGCGGGCGCCAATG  582
Sbjct  887  TGGGCTTCCTCAGGGCACTGACCCACTCCGAGCTGGACGTGCGAACGGCGGGCGCCAATG  946
Query  583  GCACGTGCGGCTTCTTCTGTGTGGACGAGGGGAGGCTGCCCCACACCCAGAGGCTGCTGG  642
Sbjct  947  GCACGTGCGGCTTCTTCTGCGTGGACGAGGGGAGGCTGCCCCACACCCAGAGGCTGCTGG  1006
Query  643  AGGTCATCTCCGTGTGTGATTGCCCCAGAGGCCGTTTCTTGCCGCCATCTGCCAAGACT  702
Sbjct  1007  AGGTCATCTCCGTGTGTGATTGCCCCAGAGGCCGTTTCTTGCCGCCATCTGCCAAGACT  1066
Query  703  GTGGCCGCGAGGAAGCTGCCCGTGGACCGCATCGTGGGAGGCCGGGACACCAAGCTTGGGCC  762
Sbjct  1067  GTGGCCGCGAGGAAGCTGCCCGTGGACCGCATCGTGGGAGGCCGGGACACCAAGCTTGGGCC  1126
Query  763  GGTGGCCGTGGCAAGTCAGCCTTCGCTATGATGGAGCACACCTCTGTGGGGGATCCCTGC  822
Sbjct  1127  GGTGGCCGTGGCAAGTCAGCCTTCGCTATGATGGAGCACACCTCTGTGGGGGATCCCTGC  1186
Query  823  TCTCCGGGGACTGGGTGCTGACAGCCGCCACTGCTTCCCGGAGCGGAACCGGGTCTGT  882
Sbjct  1187  TCTCCGGGGACTGGGTGCTGACAGCCGCCACTGCTTCCCGGAGCGGAACCGGGTCTGT  1246
Query  883  CCCGATGGCGAGTGTGTTGCCGGTGCCGTGGCCCAGGCCTCTCCCAAGGCTGCGAGCTGG  942
Sbjct  1247  CCCGATGGCGAGTGTGTTGCCGGTGCCGTGGCCCAGGCCTCTCCCAAGGCTGCGAGCTGG  1306
Query  943  GGGTGACAGGCTGTGGTCTACACGCGGGGCTATCTTCCCTTTTCGGGACCCCAACAGCGAGG  1002
Sbjct  1307  GGGTGACAGGCTGTGGTCTACACGCGGGGCTATCTTCCCTTTTCGGGACCCCAACAGCGAGG  1366
Query  1003  AGAACAGCAACGATATTGCCCTGGTCCACCTCTCCAGTCCCCTGCCCCCTACAGAATACA  1062
Sbjct  1367  AGAACAGCAACGATATTGCCCTGGTCCACCTCTCCAGTCCCCTGCCCCCTACAGAATACA  1426
Query  1063  TCCAGCCTGTGTGCCTCCAGCTGCCGGCCAGGCCCTGGTGGATGGCAAGATCTGTACCG  1122
Sbjct  1427  TCCAGCCTGTGTGCCTCCAGCTGCCGGCCAGGCCCTGGTGGATGGCAAGATCTGTACCG  1486
Query  1123  TGACGGGCTGGGGCAACACGCAGTACTATGGCCAACAGGCCGGGGTACTCCAGGAGGCTC  1182

```

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Sbjct  1487  TGACGGGCTGGGGCAACACGCAGTACTATGGCCAAACAGGCCGGGTACTCCAGGAGGCTC 1546
Query   1183  GAGTCCCCATAATCAGCAATGATGT 1207
          |||||
Sbjct  1547  GAGTCCCCATAATCAGCAATGATGT 1571

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Score = 968 bits (524), Expect = 0.0
 Identities = 528/530 (99%), Gaps = 0/530 (0%)
 Strand=Plus/Plus

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Query  1254  TTCTGTGCTGGCTACCCCGAGGGTGGCATTGATGCCTGCCAGGGCGACAGCGGTGGTCCC 1313
Sbjct  1573  TTCTGTGCTGGCTACCCCGAGGGTGGCATTGATGCCTGCCAGGGCGACAGCGGTGGTCCC 1632
Query  1314  TTTGTGTGTGAGGACAGCATCTCTCGGACGCCACGTTGGCGGCTGTGTGGCATTGTGAGT 1373
          |||||
Sbjct  1633  TTTGTGTGTGAGGACAGCATCTCTCGGACGCCACGTTGGCGGCTGTGTGGCATTGTGAGT 1692
Query  1374  TGGGGCACTGGCTGTGCCCTGGCCCAGAAGCCAGGCGTCTACACCAAAGTCAGTGACTTC 1433
          |||||
Sbjct  1693  TGGGGCACTGGCTGTGCCCTGGCCCAGAAGCCAGGCGTCTACACCAAAGTCAGTGACTTC 1752
Query  1434  CGGGAGTGGATCTTCCAGGCCATAAAGACTCACTCCGAAGCCAGCGGCATGGTGACCCAG 1493
          |||||
Sbjct  1753  CGGGAGTGGATCTTCCAGGCCATAAAGACTCACTCCGAAGCCAGCGGCATGGTGACCCAG 1812
Query  1494  CTCTGACCGGTGGCTTCTCGCTGCGCAGCCTCCAGGGCCCGAGGTGATCCCGGTGGTGGG 1553
          |||||
Sbjct  1813  CTCTGACCGGTGGCTTCTCGCTGCGCAGCCTCCAGGGCCCGAGGTGATCCCGGTGGTGGG 1872
Query  1554  ATCCACGCTGGGCGGAGGATGGGACGTTTTTCTTCTTGGGCCCGGTCCACAGGTCCAAGG 1613
          |||||
Sbjct  1873  ATCCACGCTGGGCGCTAGGATGGGACGTTTTTCTTCTTGGGCCCGGTCCACAGGTCCAAGG 1932
Query  1614  ACACCCCTCCCTCCAGGGTCCTCTCTTCCACAGTGGCGGGCCCACTCAGCCCCGAGACCAC 1673
          |||||
Sbjct  1933  ACACCCCTCCCTCCAGGGTCCTCTCTTCCACAGTGGCGGGCCCACTCAGCCCCGAGACCAC 1992
Query  1674  CCAACCTCACCTCCTGACCCCATGTAAATATTGTTCTGCTGTCTGGGACTCCTGTCTA 1733
          |||||
Sbjct  1993  CCAACCTCACCTCCTGACCCCATGTAAATATTGTTCTGCTGTCTGGGACTCCTGTCTA 2052
Query  1734  GGTGCCCTGATGACGGGATGCTCTTTAAATAATAAAGATGGTTTTGATT 1783
          |||||
Sbjct  2053  GGTGCCCTGATGACGGGATGCTCTTTAAATAATAAAGATGGTTTTGATT 2102

```

>emb|CU693028.1| Synthetic construct Homo sapiens gateway clone IMAGE:100019300
 5' read HPN mRNA
 Length=1222

Score = 1465 bits (793), Expect = 0.0
 Identities = 972/1052 (92%), Gaps = 38/1052 (3%)
 Strand=Plus/Plus

```


Query  245  CATGGCGCAGAAGGAGGGTGGCCGGAAGTGTGCCATGCTGCTCCAGACCCAAGGTGGCAGC 304
Sbjct  16  CATGGCGCAGAAGGAGGGTGGCCGGAAGTGTGCCATGCTGCTCCAGACCCAAGGTGGCAGC 75
Query  305  TCTCACTGCGGGGACCTTGCTACTTCTGACAGCCATCGGGGCGGCATCCTGGGCCATTGT 364
          |||||
Sbjct  76  TCTCACTGCGGGGACCTTGCTACTTCTGACAGCCATCGGGGCGGCATCCTGGGCCATTGT 135
Query  365  GGCTGTTCTCCTCAGGAGTGACCAGGAGCCGCTGTACCCAGTGCAGGTGAGCTCTGCGGA 424
          |||||
Sbjct  136  GGCTGTTCTCCTCAGGAGTGACCAGGAGCCGCTGTACCCAGTGCAGGTGAGCTCTGCGGA 195
Query  425  CGCTCGGCTCATGGTCTTTGACAAGACGGAAGGGACGTTGGCGGCTGCTGTGCTCCTCGCG 484
          |||||
Sbjct  196  CGCTCGGCTCATGGTCTTTGACAAGACGGAAGGGACGTTGGCGGCTGCTGTGCTCCTCGCG 255
Query  485  CTCCAACGCCAGGGTAGCCGGACTCAGCTGCGAGGAGATGGGCTTCTCAGGGCACTGAC 544
          |||||
Sbjct  256  CTCCAACGCCAGGGTAGCCGGACTCAGCTGCGAGGAGATGGGCTTCTCAGGGCACTGAC 315
Query  545  CCACTCCGAGCTGGACGTGCGAACGCGGGCGCCAATGGCACGTGGGCTTCTTCTGTGT 604
          |||||
Sbjct  316  CCACTCCGAGCTGGACGTGCGAACGCGGGCGCCAATGGCACGTGGGCTTCTTCTGTGT 375
Query  605  GGACGAGGGGAGGCTGCCCCACACCAGAGGCTGCTGGAGGTGATCTCCGTGTGTGATTG 664
          |||||
Sbjct  376  GGACGAGGGGAGGCTGCCCCACACCAGAGGCTGCTGGAGGTGATCTCCGTGTGTGATTG 435
Query  665  CCCCAGAGGCCGTTTCTTGGCCGCCATCTGCCAAGACTGTGGCCGCAGGAAGCTGCCCGT 724
          |||||
Sbjct  436  CCCCAGAGGCCGTTTCTTGGCCGCCATCTGCCAAGACTGTGGCCGCAGGAAGCTGCCCGT 495
Query  725  GGACCGCATCGTGGGAGGCCGGGACACCAGCTTGGGCCGGTGGCCGTGGCAAGTCAGCCT 784
          |||||
Sbjct  496  GGACCGCATCGTGGGAGGCCGGGACACCAGCTTGGGCCGGTGGCCGTGGCAAGTCAGCCT 555
Query  785  TCGCTATGATGGAGCACACCTCTGTGGGGGATCCCTGCTCTCCGGGGACTGGGTGCTGAC 844
          |||||
Sbjct  556  TCGCTATGATGGAGCACACCTCTGTGGGGGATCCCTGCTCTCCGGGGACTGGGTGCTGAC 615
Query  845  AGCCGCCCACTGCTTCCCGGAGCGGAACCGGGTCTGTCCCGATGGCGAGTGTTCGCCG 904
          |||||

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Sbjct  616  AGCCGCCCATTTGCTTCCCGAGCGGAACCGGGTCTGTCCCGATGGCGAGTGTTCGCCG  675
Query  905  TGCCGTGGCCCC-AGGCCTCTCCCCACGGTCTGC-AGCTGGGGGTGCAGGCTGTGGTCTAC  962
      |||
Sbjct  676  TGCCGTGGCCCCAG-CCTCTCCCCCGGTCTGCCA-CTGGGGGGGCAGGCTGTGGTCTAC  733
Query  963  CACGGGGG-CTATCTTCCCTTT-CGGGACCCCAACAGCGAGGAGAACAGCAACGA-TATT  1019
      |||
Sbjct  734  C-CGGGGGGCT-TCTTCCCTTTTCGG-ACCC-ACCCGCGAGGAGAACAGCAACGAATATT  789
Query  1020  GCC-CTGGTCCACCTCTCCAGT-CCCCT-GCCCT-CACAGAATACATCCAGCCTG-TGT  1074
      |||
Sbjct  790  GCCTC-GGTTACCTTTTCAGTTCCTTGCCTTACCCA-AATAAATCCAGCCTGGTGT  847
Query  1075  GCCT-CCCAGCT-GCCGGCCAGGCCCTGGTGA-TGGCAAGATCTGT-ACCGTGACGGGC  1130
      |||
Sbjct  848  GCCTTCCCC-CTTGCCGCCCGGGCCCGGGGGAATGCCAAGATCTGTTACCGTGACGGGC  906
Query  1131  T-GGGG-CAACACGCAGTACTATG-GCCAAACAGGCCG-GGGTACTCCAGGAGGCTCGAG-  1185
      |||
Sbjct  907  CCGGGGACA-CACCCAGTACTTTGCGC-AACCGGCCGCGGGTATTCCCGAGGTTCTAGG  964
Query  1186  TCCCC-ATAATCAGCAA-TGA-TGTCTGCAATGGCGCTGACTTCTATGGAAAC-CAGATC  1241
      |||
Sbjct  965  TCTCTATAATAA-CAAATTAATTTCTCCAATGCGCTTACCTCTCTGTAACTCCGATC  1023
Query  1242  A-AGCCCAAGATGTTCTGTGCTGG-CTACCCC  1271
      |||
Sbjct  1024  TGACCCCAACA-GTTTTTTGCTTGTCTACCCC  1054

```

>dbj|AK095160.1|  Homo sapiens cDNA FLJ37841 fis, clone BRSSN2012081, highly similar to SERINE PROTEASE HEP SIN (EC 3.4.21.-) Length=2175

GENE ID: 3249 HPN | hepsin (transmembrane protease, serine 1) [Homo sapiens]
(Over 10 PubMed links)

Sort alignments for this subject sequence by:
E value Score Percent identity
Query start position Subject start position

Score = 1404 bits (760), Expect = 0.0
Identities = 765/767 (99%), Gaps = 1/767 (0%)
Strand=Plus/Plus

```

Query  695  CCA-AGACTGTGGCCGAGGAAGCTGCCCCGTGGACCGCATCGTGGGAGGCCGGGACACCA  753
      |||
Sbjct  870  CCACAGACTGTGGCCGAGGAAGCTGCCCCGTGGACCGCATCGTGGGAGGCCGGGACACCA  929
Query  754  GCTTGGGCGCGTGGCCGTGGCAAGTCAAGCTTCGCTATGATGGAGCACACCTCTGTGGGG  813
      |||
Sbjct  930  GCTTGGGCGCGTGGCCGTGGCAAGTCAAGCTTCGCTATGATGGAGCACACCTCTGTGGGG  989
Query  814  GATCCCTGCTCTCCGGGACTGGGTGCTGACAGCCGCCCACTGCTTCCCGAGCGGAACC  873
      |||
Sbjct  990  GATCCCTGCTCTCCGGGACTGGGTGCTGACAGCCGCCCACTGCTTCCCGAGCGGAACC  1049
Query  874  GGGTCCTGTCCCGATGGCGAGTGTTTGCCGGTGGCGTGGCCAGGCCCTCTCCCAACGGTC  933
      |||
Sbjct  1050  GGGTCCTGTCCCGATGGCGAGTGTTTGCCGGTGGCGTGGCCAGGCCCTCTCCCAACGGTC  1109
Query  934  TGCAGCTGGGGGTGCAGGCTGTGGTCTACCACGGGGGCTATCTTCCCTTTCGGGACCCCA  993
      |||
Sbjct  1110  TGCAGCTGGGGGTGCAGGCTGTGGTCTACCACGGGGGCTATCTTCCCTTTCGGGACCCCA  1169
Query  994  ACAGCGAGGAGAACAGCAACGATATGCCCCTGGTCCACCTCTCCAGTCCCCTGCCCTCA  1053
      |||
Sbjct  1170  ACAGCGAAGAGAACAGCAACGATATGCCCCTGGTCCACCTCTCCAGTCCCCTGCCCTCA  1229
Query  1054  CAGAATACATCCAGCCTGTGTGCTCCAGCTGCCGGCCAGGCCCTGGTGGATGGCAAGA  1113
      |||
Sbjct  1230  CAGAATACATCCAGCCTGTGTGCTCCAGCTGCCGGCCAGGCCCTGGTGGATGGCAAGA  1289
Query  1114  TCTGTACCGTGACGGGCTGGGGCAACACGCACTACTATGGCCAAACAGGCCGGGTACTCC  1173
      |||
Sbjct  1290  TCTGTACCGTGACGGGCTGGGGCAACACGCACTACTATGGCCAAACAGGCCGGGTACTCC  1349
Query  1174  AGGAGGCTCGAGTCCCCATAATCAGCAATGATGTCTGCAATGGCGCTGACTTCTATGGAA  1233
      |||
Sbjct  1350  AGGAGGCTCGAGTCCCCATAATCAGCAATGATGTCTGCAATGGCGCTGACTTCTATGGAA  1409
Query  1234  ACCAGATCAAGCCCAAGATGTTCTGTGCTGGCTACCCCGAGGGTGGCATTGATGCCTGCC  1293
      |||
Sbjct  1410  ACCAGATCAAGCCCAAGATGTTCTGTGCTGGCTACCCCGAGGGTGGCATTGATGCCTGCC  1469
Query  1294  AGGGCGACAGCGGTGGTCCCTTTGTGTGTGAGGACAGCATCTCTCGGACGCCACGTTGGC  1353
      |||
Sbjct  1470  AGGGCGACAGCGGTGGTCCCTTTGTGTGTGAGGACAGCATCTCTCGGACGCCACGTTGGC  1529
Query  1354  GGCTGTGTGGCATTGTGAGTTGGGGCACTGGCTGTGCCCTGGCCCAGAAGCCAGGCGTCT  1413
      |||
Sbjct  1530  GGCTGTGTGGCATTGTGAGTTGGGGCACTGGCTGTGCCCTGGCCCAGAAGCCAGGCGTCT  1589
Query  1414  ACACCAAAGTCAGTGACTTCCGGGAGTGGATCTTCCAGGCCATAAAG  1460
      |||
Sbjct  1590  ACACCAAAGTCAGTGACTTCCGGGAGTGGATCTTCCAGGCCATAAAG  1636

```

Score = 601 bits (325), Expect = 4e-168
 Identities = 325/325 (100%), Gaps = 0/325 (0%)
 Strand=Plus/Plus

```

Query 1459 AGACTCACTCCGAAGCCAGCGGCATGGTGACCCAGCTCTGACCGGTGGCTTCTCGCTGCG 1518
          |||
Sbjct 1851 AGACTCACTCCGAAGCCAGCGGCATGGTGACCCAGCTCTGACCGGTGGCTTCTCGCTGCG 1910

Query 1519 CAGCCTCCAGGGCCCGAGGTGATCCCGGTGGTGGGATCCACGCTGGGCCGAGGATGGGAC 1578
          |||
Sbjct 1911 CAGCCTCCAGGGCCCGAGGTGATCCCGGTGGTGGGATCCACGCTGGGCCGAGGATGGGAC 1970

Query 1579 GTTTTCTCTTCTTGGGCCCGGTCCACAGGTCCAAGGACACCCCTCCCTCCAGGGTCCTCTCT 1638
          |||
Sbjct 1971 GTTTTCTCTTCTTGGGCCCGGTCCACAGGTCCAAGGACACCCCTCCCTCCAGGGTCCTCTCT 2030

Query 1639 TCCACAGTGGCGGGCCCACTCAGCCCCGAGACCACCCAACTCACCCTCCTGACCCCCAT 1698
          |||
Sbjct 2031 TCCACAGTGGCGGGCCCACTCAGCCCCGAGACCACCCAACTCACCCTCCTGACCCCCAT 2090

Query 1699 GTAAATATTGTTCTGCTGTCTGGGACTCCTGTCTAGGTGCCCTGATGATGGGATGCTCT 1758
          |||
Sbjct 2091 GTAAATATTGTTCTGCTGTCTGGGACTCCTGTCTAGGTGCCCTGATGATGGGATGCTCT 2150

Query 1759 TTAAATAATAAAGATGGTTTTGATT 1783
          |||
Sbjct 2151 TTAAATAATAAAGATGGTTTTGATT 2175
  
```

Score = 322 bits (174), Expect = 4e-84
 Identities = 174/174 (100%), Gaps = 0/174 (0%)
 Strand=Plus/Plus

```

Query 363 GTGGCTGTTCTCCTCAGGAGTGACCAGGAGCCGCTGTACCCAGTGACAGGTGAGCTCTGCG 422
          |||
Sbjct 159 GTGGCTGTTCTCCTCAGGAGTGACCAGGAGCCGCTGTACCCAGTGACAGGTGAGCTCTGCG 218

Query 423 GACGCTCGGCTCATGGTCTTTGACAAGACGGAAGGGACGTGGCGGCTGCTGTGCTCCTCG 482
          |||
Sbjct 219 GACGCTCGGCTCATGGTCTTTGACAAGACGGAAGGGACGTGGCGGCTGCTGTGCTCCTCG 278

Query 483 CGCTCCAACGCCAGGGTAGCCGGACTCAGCTGCGAGGAGATGGGCTTCCTCAGG 536
          |||
Sbjct 279 CGCTCCAACGCCAGGGTAGCCGGACTCAGCTGCGAGGAGATGGGCTTCCTCAGG 332
  
```

Score = 233 bits (126), Expect = 2e-57
 Identities = 129/130 (99%), Gaps = 1/130 (0%)
 Strand=Plus/Plus

```

Query 533 CAGGGCACTGACCCACTCCGAGCTGGACGTGCGAACGGCGGGCGCCAATGGCACGTCGGG 592
          |||
Sbjct 400 CAGGGCACTGACCCACTCCGAGCTGGACGTGCGAACGGCGGGCGCCAATGGCACGTCGGG 459

Query 593 CTTCTTCTGTGTGGACGAGGGGAGGCTGCCCCACACCCAGAGGCTGCTGGAGGTCATCTC 652
          |||
Sbjct 460 CTTCTTCTGTGTGGACGAGGGGAGGCTGCCCCACACCCAGAGGCTGCTGGAGGTCATCTC 519

Query 653 CGTGTG-TGA 661
          |||
Sbjct 520 CGTGTGGTGA 529
  
```

Score = 141 bits (76), Expect = 1e-29
 Identities = 76/76 (100%), Gaps = 0/76 (0%)
 Strand=Plus/Plus

```


Query 288 AGACCCAAGGTGGCAGCTCTCACTGCGGGGACCCCTGCTACTTCTGACAGCCATCGGGGCG 347
          |||
Sbjct 1 AGACCCAAGGTGGCAGCTCTCACTGCGGGGACCCCTGCTACTTCTGACAGCCATCGGGGCG 60

Query 348 GCATCCTGGGCCATTG 363
          |||
Sbjct 61 GCATCCTGGGCCATTG 76
  
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Score = 78.7 bits (42), Expect = 9e-11
 Identities = 42/42 (100%), Gaps = 0/42 (0%)
 Strand=Plus/Plus

```

Query 658 GTGATTGCCCCAGAGGCCGTTTCTTGGCCGCCATCTGCCAAG 699
          |||
Sbjct 657 GTGATTGCCCCAGAGGCCGTTTCTTGGCCGCCATCTGCCAAG 698
  
```

>ref|XM_001093460.1|  PREDICTED: Macaca mulatta hepsin (transmembrane protease, serine 1), transcript variant 1 (HPN), mRNA
 Length=2174

GENE ID: 707242 HPN | hepsin (transmembrane protease, serine 1)
 [Macaca mulatta]

Sort alignments for this subject sequence by:
 E value Score Percent identity
 Query start position Subject start position

Score = 1360 bits (736), Expect = 0.0
 Identities = 757/767 (98%), Gaps = 1/767 (0%)
 Strand=Plus/Plus

```

Query   695   CCA-AGACTGTGGCCGAGGAAGCTGCCCCGTGGACCGCATCGTGGGAGGCCGGGACACCA   753
Sbjct   867   CCACAGACTGTGGCCGAGGAAGCTGCCCCGTGGACCGCATCGTGGGAGGCCGGGACACCA   926

Query   754   GCTTGGGCGCGTGGCCGTGGCAAGTCAGCCTTCGCTATGATGGAGCACACCTCTGTGGGG   813
Sbjct   927   GCTTGGGCGCGTGGCCGTGGCAAGTCAGCCTTCGCTATGATGGAGCACACCTCTGTGGGG   986

Query   814   GATCCCTGCTCTCCGGGACTGGGTGCTGACAGCCGCCCACTGCTTCCCGAGCGGAACC   873
Sbjct   987   GGTCCCTGCTCTCCGGGACTGGGTGCTGACAGCTGCCCACTGCTTCCCGAGCGGAACC   1046

Query   874   GGGTCCTGTCCCGATGGCGAGTGTGTTGCCGGTGGCGTGGCCAGGCCCTCTCCCCACGGTC   933
Sbjct   1047  GGGTCCTGTCCCGATGGCGAGTGTGTTGCCGGTGGCGTGGCCAGGCCCTCTCCCCACGGCC   1106

Query   934   TGCAGCTGGGGGTGCAGGCTGTGGTCTACCAAGGGGGCTATCTTCCCTTTCGGGACCCCA   993
Sbjct   1107  TGCAGCTGGGGGTGCAGGCTGTGGTCTACCAAGGGGGCTATCTTCCCTTTCGGGACCCCA   1166

Query   994   ACAGCGAGGAGAAACAGCAACGATATTGCCCTGGTCCACCTCTCCAGTCCCCCTGCCCTCA   1053
Sbjct   1167  ACAGCGAGGAGAAACAGCAATGATATTGCCCTGGTCCACCTCTCCAGTCCCCCTGCCCTCA   1226

Query   1054  CAGAATACATCCAGCCTGTGTGCCTCCCAGCTGCCGGCCAGGCCCTGGTGGATGGCAAGA   1113
Sbjct   1227  CAGAATACATCCAGCCTGTGTGCCTCCCAGCTGTGGCCAGGCCCTGGTGGATGGCAAGA   1286

Query   1114  TCTGTACCGTGACGGGCTGGGGCAACACGCAGTACTATGGCCAAACAGGCCGGGGTACTCC   1173
Sbjct   1287  TCTGTACCGTGACGGGCTGGGGCAACACGCAGTACTATGGCCAAACAGGCCGGGGTACTCC   1346

Query   1174  AGGAGGCTCGAGTCCCCATAATCAGCAATGATGTCTGCAATGGCGCTGACTTCTATGGAA   1233
Sbjct   1347  AGGAGGCTCGAGTCCCCATAATCAGCAATGATGTCTGCAATGGCGCTGACTTCTATGGAA   1406

Query   1234  ACCAGATCAAGCCCAAGATGTTCTGTGCTGGCTACCCCGAGGGTGGCATTGATGCCTGCC   1293
Sbjct   1407  ACCAGATCAAGCCCAAGATGTTCTGTGCTGGCTACCCCGAGGGTGGCATTGATGCCTGCC   1466

Query   1294  AGGGCGACAGCGGTGGTCCCTTGTGTGTGAGGACAGCATCTCTCGGACGCCACGTTGGC   1353
Sbjct   1467  AGGGTGACAGCGGTGGTCCCTTGTGTGTGAGGACAGCATCTCTCGGACGCCACGTTGGC   1526

Query   1354  GGCTGTGTGGCATTGTGAGTTGGGGCACTGGCTGTGCCCTGGCCCAGAAGCCAGGCGTCT   1413
Sbjct   1527  GGCTGTGTGGCATTGTGAGCTGGGGCACTGGCTGTGCCCTGGCCCAGAAGCCAGGCGTCT   1586

Query   1414  ACACCAAAGTCAGTGACTTCCGGGAGTGGATCTTCCAGGCCATAAAG   1460
Sbjct   1587  ACACCAAAGTCAGTGACTTCCGGGAGTGGATCTTCCAGGCCATAAAG   1633

```

Score = 551 bits (298), Expect = 4e-153
 Identities = 316/325 (97%), Gaps = 0/325 (0%)
 Strand=Plus/Plus

```

Query   1459  AGACTCACTCCGAAGCCAGCGGCATGGTGACCCAGCTCTGACCGGTGGCTTCTCGCTGCG   1518
Sbjct   1848  AGACTCACTCCGAAGCCAGCGGCATGGTGACCCAGCTCTGACCGGTGGCTTCTCGCTGCG   1907

Query   1519  CAGCCTCCAGGGCCCGAGGTGATCCCGGTGGTGGGATCCACGCTGGGCCGAGGATGGGAC   1578
Sbjct   1908  CAGCCTCCAGGGCCCGAGGTGATCTTGGTGGTGGGATCCACGCTGGGCCCTAGGATGGGAC   1967

Query   1579  GTTTTTCTTCTTGGGCCCGGTCCACAGGTCCAAGGACACCCCTCCCTCCAGGGTCTCTCT   1638
Sbjct   1968  ATTTTTCTTCTTGGGCCCGGTCCACAGGTCCAAGGACACCCCTCCCTCCAGGGTCTCTTCT   2027

Query   1639  TCCACAGTGGCGGGCCCACTCAGCCCCGAGACCACCAACCTCACCTCCTGACCCCCAT   1698
Sbjct   2028  TCCACAGTGGCGGGCCCACTCAGCCCCGAGACCACCGACCTCACCTCCTGACCCCCGT   2087

Query   1699  GTAAATATTGTTCTGCTGTCTGGGACTCCTGTCTAGGTGCCCTGATGATGGGATGCTCT   1758
Sbjct   2088  GTAAATATTGTTCTGCTGTCTGGGACTCCTGTCTAGGTGCCCTGATGACGGGATGCTCT   2147

Query   1759  TTAAATAATAAAGATGGTTTTGATT   1783
Sbjct   2148  TTAAATAATAAAGATGGTTTTGATT   2172

```

Score = 300 bits (162), Expect = 2e-77
 Identities = 170/174 (97%), Gaps = 0/174 (0%)
 Strand=Plus/Plus

```

Query   363   GTGGCTGTTCTCCTCAGGAGTGACCAGGAGCCGCTGTACCCAGTGACAGGTCTGCG   422
Sbjct   158   GTGGCTGTTCTCCTCAGGAGTGACCAGGAGCCGCTGTACCCAGTGACAGGTCTGCG   217

Query   423   GACGCTCGGCTCATGGTCTTTGACAAGACGGAAGGACGTGGCGGCTGCTGTGCTCCTCG   482
Sbjct   218   GACGCTCGGCTCATGGTCTTTGACAAGACGGAAGGACGTGGCGGCTGCTATGCTCCTCA   277

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```

Query   483  CGCTCCAACGCCAGGGTAGCCGGAAGTGCAGGAGATGGGCTTCCTCAGG  536
Sbjct   278  CGCTCCAACACCAGGGTAGCCGGAAGTGCAGGAGATGGGCTTCCTCAGG  331

```

Score = 206 bits (111), Expect = 4e-49
 Identities = 124/130 (95%), Gaps = 1/130 (0%)
 Strand=Plus/Plus

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Query   533  CAGGGCACTGACCCACTCCGAGCTGGACGTGCGAACGGCGGGCGCCAATGGCACGTCGGG  592
Sbjct   399  CAGGGCACTGACCCACTCCGAGTTGGACGTGCGAACGGCGGGCGCCAACGGCACGTCAGG  458

Query   593  CTTCTTCTGTGTGGACGAGGGGAGGCTGCCCCACACCCAGAGGCTGCTGGAGGTCATCTC  652
Sbjct   459  CTTCTTCTGTGTGGATGAGGGGAGGCTGCCACACACCCAGAGGCTGCTGGAGGTCATCTC  518

Query   653  CGTGTG-TGA  661
Sbjct   519  CGTGTGGTGA  528

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Score = 134 bits (72), Expect = 2e-27
 Identities = 74/75 (98%), Gaps = 0/75 (0%)
 Strand=Plus/Plus

```

Query   289  GACCCAAGGTGGCAGCTCTCACTGCGGGGACCTGCTACTTCTGACAGCCATCGGGGCGG  348
Sbjct    1  GACCCAAGGTGGCAGCTCTCACTGCGGGGACCTGCTACTTCTGACAGCCATCGGGGCGG  60

Query   349  CATCCTGGGCCATTG  363
Sbjct   61  CATCCTGGGCCATTG  75

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>ref|NM_008281.3|  Mus musculus hepsin (Hpn), transcript variant 2, mRNA
 Length=1770

GENE ID: 15451 Hpn | hepsin [Mus musculus] (Over 10 PubMed links)

Score = 1303 bits (705), Expect = 0.0
 Identities = 1343/1644 (81%), Gaps = 71/1644 (4%)
 Strand=Plus/Plus

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Query   184  ACCCCAGGGTCCCACCTGGCCCAGGAGGTCAGCCAGGGAATCATTAAACAAGAGGCAGTG  243
Sbjct   148  ACCCCAGGGTTCCGCCCCAGCCCAACAGGTCAACCTGGGAATCATTAAACAAGAGTCCCTG  207

Query   244  ACATGGCGCAGAAGGAGGGTGGCCGGAAGT-TGCCATGCTGCTCCAGACCCAAGGTGGCA  302
Sbjct   208  ACAT-G-GC-GAAGGAGGGTGGCCGGAAGT-CATGCTGCTCCAGACCCAAGGTGGCA  263

Query   303  GCTCTCACTGCGGGGACCTGCTACTTC-TGACAGCCATCGGGGCGGCATCTGGGCCAT  361
Sbjct   264  GCTCTCATTGTGGGTACCTGCTG-TTCCTGACAGGCATTGGGGCGCGTCTCTGGGCCAT  322

Query   362  TGTGGCTGTTCTCCT-CAGGAGTGACAGGAGCCGCTGTACCCAGTGCAGGTCAGCTCT-  419
Sbjct   323  TGTGACCATCTACTGAG-AGTGACAGGAGCCACTGTACCAAGTGCAGCTCAG-TCCA  380

Query   420  GCGGACGCTCGGCTCATGGTCTTTGACAAGACGGAAGGGA-CGTGGCGGCTGCTGTGCTC  478
Sbjct   381  GGGGACTCACGGCTTGCAGGTGTTTGACAAGACGGA-GGGAACGTGGAGGCTACTGTGCTC  439

Query   479  CTCGCGCTCCAACGCCAGGGTAGCCGGAAGTGCAGGAGATGGGCTTCCTCAGGGC  538
Sbjct   440  CTCACGCTCCAATGCCAGGGTGGCAGGGCTCGGCTGTGAGGAGATGGGCTTCTCAGGGC  499

Query   539  ACTGACCCACTCCGAGCTGGACGTGCGAACGGCGGGCGCCAATGGCACGTCGGGCTTCTT  598
Sbjct   500  TCTGGCGCACTCGGAGCTGGATGTGCGCACTGCGGGCGCCAACGGCACATCGGGCTTCTT  559

Query   599  CTGTGTGGACGAGGGGAGG-CTGCCCCACACCCAGAGGCTGCTGGAGGTCTCTCCGTGT  657
Sbjct   560  TTGCGTGGACGAGGGC-GGACTGCCTCTGGCTCAGAGGTGCTGGATGTCATCTGTAT  618

Query   658  GTGATTGCCCCAGAGGCCGTTTCTTGGCCGCCATCTGCCAAGACTGTGGCCGAGGAAGC  717
Sbjct   619  GTGACTGTCTAGAGGCCGATTCTCTGACTGCCACTGCCAAGACTGTGGCCGAGGAAGC  678

Query   718  TGCCCGTGGACCGCATCGTGGGAGGCCGGACACAG-CTTGGGCCGCTGGCCGTGGCAA  776
Sbjct   679  TGCCCGTGGACCGCATTGTGGGGGGCCAGGACAGCAGTCT-GGGAAGGTGGCCGTGGCAG  737

Query   777  GTCAGCCTTCGCTATGATGG-AGCACACCTCTGTGGGGGATCCCTGCTCTCCGGGGACTG  835
Sbjct   738  GTCAGCCTGCGTTATGATGGGACC-CACCTCTGTGGGGGTCCCTGCTGTCTGGGGACTG  796

Query   836  GGTGCTGACAGCCGCCCACTGCTTCCCGGAGCGGAACCGGGTCTGTCCCGATGGCGAGT  895
Sbjct   797  GGTGCTGACTGTGTCACATTGCTTTCCAGAGCGGAACCGGGTCTGTCTCGGTGGCGAGT  856

Query   896  GTTTGCCCGTGGCTGGCCAGG-CCTCTCCACAGTCTGCAGCTGGGGGTGCAGGCTG  954
Sbjct   857  ATTTGCTGGTGTGTAGCCC-GGACCTCACCCCATGCTGTGCAACTGGGGGTTCAGGCTG  915

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Query 955  TGGTCTACCAACGGGGGCTATCTTCCCTTTTCGGGACCCCAAC-AGCGAGGAGAACAGCAAC 1013
Sbjct 916  TGATCTATCATGGGGGCTACCTTCCCTTTTCGAGACCCCTA-CTATCGACGAAAAAGCAAT 974

Query 1014  GATATTGCCCTGGTCCACCTCTCCAG-TCCCCCTGCCCCCTACAGAATACATCCAGCCTGT 1072
Sbjct 975  GACATTGCCCTGGTCCACCTCTCTAGCTCCC-TGCCTCTCACAGAATACATCCAGCCAGT 1033

Query 1073  GTGCTCTCCAGCTGCCGGCCAGGCCCTGGTGGATGGCAAGATCTGTACCGTGACGGGCTG 1132
Sbjct 1034  GTGTCTCCCTGTGTCGGGACAGGCCCTGGTGGATGGCAAGGTCTGTACTGTGACCGGCTG 1093

Query 1133  GGGCAACACGCAGTACTATGGCCAACAGGCCGGGTAATCCAGGAGGCTCGAGTCCCCAT 1192
Sbjct 1094  GGGTAACACACAGTTCTATGGCCAACAGGCTATGGTGCTCCAAGAGGCCCGGGTTCCCAT 1153

Query 1193  AATCAGCAATGATGTCTGCAATGGCGCTGACTTCTATGGAAACAGATCAAGCCCCAAGAT 1252
Sbjct 1154  CATAAGCAACGAAGTTTGCAACAGCCCCGACTTCTACGGGAATCAGATCAAGCCCCAAGAT 1213

Query 1253  GTTCTGTGCTGGCTACCCGAGGGTGGCATTGATGCCTGCCAGGGCGACAGCGGTGGTCC 1312
Sbjct 1214  GTTCTGTGCTGGCTATCTGAGGGTGGCATTGATGCGTGCCAGGGCGACAGTGGAGGGCC 1273

Query 1313  CTTTGTGTGTGAGGACAGCATCTCTCGGACGCCACGTTGGCGGCTGTGTGGCATTGTGAG 1372
Sbjct 1274  CTTTGTGTGTGAAGACAGCATCTCTGGGACATCAAGGTGGCGCTATGTGGCATTGTAAG 1333

Query 1373  TTGGGGCACTGGCTGTGCCCTGGCCAGAAAGCCAGGCGTCTACACAAAGTCAGTGACTT 1432
Sbjct 1334  CTGGGGTACGGGCTGTGCTTTGGCCCGGAAGCCAGGAGTGTAACACAAAGTCACTGACTT 1393

Query 1433  CCGGGAGTGGATCTTCCAGGCCATAAAGACTCACTCCGAAGCCAGCGCATGGTGACCCA 1492
Sbjct 1394  CCGGGAGTGGATCTTCAAGGCCATAAAGACTCACTCCGAAGCCAGTGGCATGGTGACTCA 1453

Query 1493  GCTCTGA-CCGG--TGG-CT---T-CTC-G--CTGCGC-AGCCTCCAGGGCCCGAG--G- 1537
Sbjct 1454  GCCCTGATCCCGCCTCATCTCGCTGCTCCGTGCTGCACTAGCATCCAGAGTCAGAGTTGG 1513

Query 1538  T--GAT--C-CC-G-----GTGGTGGGATCCACGCTGGGCCG-AGGATGGGACGTTTTT 1584
Sbjct 1514  TCTGGTGGCTCCAGCCCCACGTGGTAGGCTCCACACTGGGCCTCAC-ATGGAATGGTTTC 1572


Query 1585  CTTCTTGGGCCCCGTCCACAGGTCCAAGGACACCTCCCTCCAGGGTCCTCTCTTCCACA 1644
Sbjct 1573  CTGCTCAGATCCAGTCCACGGGTCCAAGGATGC--TGATCCAAGGACTTCTCTTCCACA 1630


Query 1645  GTGGCGGGCCCACTCAGCCCC-GAGACCACCAACCTCACCTCCTGACCCCCATGTAAA 1703
Sbjct 1631  GTGGCCGGCCCACTCAATCCAGGG-CCATTGG-CCTCACCTCCC-ACCCC-ATGTAAA 1686

Query 1704  TATTGTTCTG-CTGTCTGGGACTC-CTGTCTAGGT-GCCCCTGATGATGG-GATGCTCTT 1759
Sbjct 1687  TATTACTCTGTCC-TCTGGGGGGCGCT--CTAGGGAGCCCCCT--TG-TGCAGATGCTCTT 1740

Query 1760  TAAATAATAAAGATGGTTTTGATT 1783
Sbjct 1741  TAAATAATAAAGGTGGTTTTGATT 1764

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>ref|NM_017112.1|  Rattus norvegicus hepsin (Hpn), mRNA

emb|X70900.1|RNHEPA  R.norvegicus mRNA for hepsin
Length=1739

GENE ID: 29135 Hpn | hepsin [Rattus norvegicus] (10 or fewer PubMed links)

Score = 1297 bits (702), Expect = 0.0
Identities = 1341/1643 (81%), Gaps = 69/1643 (4%)
Strand=Plus/Plus

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Query 184  ACCCCAGGGTCCCACCTGGCCAGGAGTCCAGCCAGGGAATCATTAAACAAGAGGCAGTG 243
Sbjct 123  ACCCCAGGGTTCCGCCCCAGCCCAACAGGTCAACCTGGGAATCATTAAACAAGAGTCCCTG 182

Query 244  ACATGGCGCAGAAGGAGGGTGGCCGGAAGTGTGCCATGCTGCTCCAGACCCAAGGTGGCAG 303
Sbjct 183  ACAT-G-GC-GAAGGAGGGTGGCCGGAAGTGCACCATGCTGTTCCAGACCCAAGGTGGCAG 239

Query 304  CTCTCACTGCGGGGACCTGCTACTTC-TGACAGCCATCGGGGCGGCATCCTGGGGCCATT 362
Sbjct 240  CTCTCACTGTGGGGACCTGCTG-TTCCTGACAGGCATTGGGGCTGCGTCTCTGGGGCCATT 298

Query 363  GTGGCTGTTCTCCT-CAGGAGTGACCAGGAGCCGCTGTACCCAGTGCCAGGTCAG-CTCTG 420
Sbjct 299  GTGACCATCCTACTAC-GGAGTGACCAGGAGCCACTGTACCAAGTGAGCTCAGTCCCGG 357

Query 421  CGGACGCTCGGCTCATGGTCTTTGACAAGACGGAAGGGA-CGTGGCGGCTGCTGTGCTCC 479
Sbjct 358  -GGACTCTCGACTTTTGGTGTGGACAAGACAGA-GGGAACGTGGAGGCTGCTGTGCTCC 415

Query 480  TCGCGCTCCAACGCCAGGGTAGCCGGAAGTCCAGTGCGAGGAGATGGGCTTCTCTAGGGCA 539
Sbjct 416  TCACGCTCCAACGCCAGGGTAGCAGGGCTCGGCTGTGAGGAGATGGGCTTTCTCAGGGCT 475


Query 540  CTGACCCACTCCGAGCTGGACGTGCGAACGGCGGGCGCCAATGGCACGTGCGGCTTCTTC 599

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Sbjct  476  CTGGCGCACTCAGAGCTGGATGTGCGAACCGCGGGCGCCAAACGGCACATCGGGCTTCTTC 535
Query  600  TGTGTGGACGAGGGGAGG-CTGCCCCACACCCAGAGGCTGCTGGAGGTCTATCTCCGTGTG 658
Sbjct  536  TGCCTGGACGAGGGG-GGTCTGCCTCTGGCTCAGCGGTTGCTGGATGTCATCTCTGTATG 594
Query  659  TGATTGCCCCAGAGGCCGTTTCTTGGCCGCCATCTGCCAAGACTGTGGCCGCAGGAAGCT 718
Sbjct  595  CGACTGTCTTAGAGGCCGATTCTGACTGCCACCTGCCAAGACTGTGGCCGCAGGAAGCT 654
Query  719  GCCCGTGGACCGCATCGTGGGAGGCCGGGACACCAGCTTGGGCCGCTGGCCGTGGCAAGT 778
Sbjct  655  GCCCGTGGATCGCATTGTGGGGGGCAGGACAGCAGCCTGGGAAGATGGCCATGGCAGGT 714
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Sbjct  715  CAGCCTGCGTTATGATGGGACC-CACCTCTGTGGGGGATCCCTGCTGTCCGGGGACTGGG 773
Query  838  TGCTGACAGCCGCCCCTGCTTCCCGAGCGGAACCGGGTCTGTCCCGATGGCGAGTGT 897
Sbjct  774  TACTGACCGCTGCACACTGCTTTCAGAGAGGAACCGGGTCTGTCTCGGTGGCGAGTAT 833
Query  898  TTGCCGGTGGCCGTGGCCCAAG-CCTCTCCCACGGTC-TGCAGCTGGGGGTGCAGGCTGT 955
Sbjct  834  TTGTGTGTGCTGTAGCCC-GGACCTCACCTCATGC-CGTGCAGCTGGGGGTTCAGGCTGT 891
Query  956  GGTCTACACGCGGGGCTATCTTCCCTTTCGGGACCCCAAC-AGCGAGGAGAACAGCAACG 1014
Sbjct  892  GATCTATCATGGGGGCTACCTTCCCTTTCGAGACCCCTA-CTATCGACGAAAAACAGCAATG 950
Query  1015  ATATTGCCCTGGTCCACCTCTCCAG-TCCCTGCCCCCTCACAGAATACATCCAGCCTGTG 1073
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Query  1074  TGCCTCCAGCTGCCGGCCAGGCCCTGGTGGATGGCAAGATCTGTACCGTGACGGGCTGG 1133
Sbjct  1010  TGTCTCCCTGCTGCGGGACAGGCCCTGGTGGACGGCAAGGTCTGTACAGTGACCGGCTGG 1069
Query  1134  GGCAACACGCAGTACTATGGCCAACAGGCCGGGGTACTCCAGGAGGCTCGAGTCCCCATA 1193
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Sbjct  1130  ATAAGCAACGAAGTTTGCAACAGCCCCGACTTCTACGGGAATCAGATCAAAACCAAGATG 1189
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Sbjct  1190  TTCTGTGCTGGCTATCCTGAGGGTGGTATTGATGCATGCCAGGGTGACAGCGGAGG-CCA 1248
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Query  1432  TCCGGGAGTGGATCTTCCAGGCCATAAAGACTCACTCCGAAGCCAGCGGCATGGTGACCC 1491
Sbjct  1368  TCCGGGAGTGGATCTTCCAGGCCATAAAGACTCACTCCGAAGCTACCGGCATGGTAACTC 1427
Query  1492  AGCTCTGACCG-G--TG--GCTT-CTC-GC--TGCGC-AGCCTCCAGGGCCCGAG--G- 1537
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Sbjct  1488  TCTGGTGGCTCCAGCCGCACGTGGCAGGCTCCACACTGGGCCTCAC-ATGGAACGGTTTT 1546
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Sbjct  1547  CTGTCGGATCCAGTCCATAGATCCAAGGATGC--TGGGTCCAAGGACCTCTCTTCCACA 1604
Query  1645  GTGGCGGGCCCACTCAGCCCC-GAGACCACCAACCTCACCTCCTGACCCCCATGTAAA 1703
Sbjct  1605  GTGGCCGGCCCACTCAATCCAGGG-CCATTGG-CCTCACCTCCC-ACCCC-ATGTAAA 1660
Query  1704  TATTGTTCTG-CTGTCTGGGA-CTCCTGTCTAGGTGCCCCCTGATGATG-GGATGCTCTTT 1760
Sbjct  1661  TATTACTCTGTCC-TCTGGGGCTGCTTTCGAGGCGCCCT--TG-TGCGGATGCTCTTT 1716
Query  1761  AAATAATAAAGATGGTTTTGATT 1783
Sbjct  1717  AAATAATAAAGTGGTTTTGATT 1739

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>gb|AF030065.1|AF030065  Mus musculus serine protease hepsin mRNA, complete cds
Length=1781

GENE ID: 15451 Hpn | hepsin [Mus musculus] (Over 10 PubMed links)

Score = 1280 bits (693), Expect = 0.0
Identities = 1341/1646 (81%), Gaps = 75/1646 (4%)
Strand=Plus/Plus

Query 184 ACCCCAGGGTCCCCACCTGGCCAGGAGGTCAGCCAGGGAATCATTAACAAGAGGCAGTG 243

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Sbjct  143  |||||CCAGGGTTCCGCCCCAGCCCAACAGGTCAACCTGGGAATCATTAAACAAGAGTCCCTG 202
Query  244  ACATGGCGCAGAAGGAGGGTGGCCGGA CTG-TGCCATGCTGCTCCAGACCCAAGGTGGCA 302
Sbjct  203  ACAT-G-GC-GAAGGAGGGTGGCCGGA CTGAG-CATGCTGCTCCAGACCCAAGGTGGCA 258
Query  303  GCTCTCACTGCGGGGACCCTGCTACTTC-TGACAGCCATCGGGGCGGCATCCTGGGCCAT 361
Sbjct  259  GCTCTCATTGTGGGTACCCCTGCTG-TTCTGACAGGCATTGGGGCCGCGTCCTGGGCCAT 317
Query  362  TGTGGCTGTTCTCCT-CAGGAGTGACAGGAGCCGCTGTACCCAGTGCAGGTGAGCTCT- 419
Sbjct  318  TGTGACCATCCTACTGAG-AGTGACAGGAGCCACTGTACCAAGTGCAGCTCAG-TCCA 375
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Sbjct  376  GGGGACTCACGACTTGCA-G-TGTTGGACAAGACGGA-GGGTACGTGGAGGCTACTGTGC 432
Query  477  TCCTCGCGCTCCAACGCCAGGGTAGCCGGA CTGAGTGCAGGAGATGGGCTTCCTCAGG 536
Sbjct  433  TCCTCACGCTCCAATGCCAGGGTGGCAGGCTCGGCTGTGAGGAGATGGGCTTTCTCAGG 492
Query  537  GCACTGACCCACTCCGAGCTGGACGTGCGAACGGCGGGCGCCAATGGCACGTCGGGCTTC 596
Sbjct  493  GCTCTGGCGCACTCGGAGCTGGATGTGCGCA CTGCGGGCGCCAACGGCACATCGGGCTTC 552
Query  597  TTCTGTGTGGACGAGGGGAGG-CTGCCCCACACCCAGAGGCTGCTGGAGGTGATCTCCGT 655
Sbjct  553  TTTTGCGTGGACGAGGGC-GGACTGCTCTGGCTCAGAGGTGCTGGATGTGATCTCTGT 611
Query  656  GTGTGATTGCCCCAGAGGCCGTTTCTTGCCGCGCATCTGCCAAGACTGTGGCCGAGGAA 715
Sbjct  612  ATGTGACTGTCTTAGAGGCCGATTCTGACTGCCACCTGCCAAGACTGTGGCCGAGGAA 671
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Sbjct  850  GTATTTGCTGCTGCTGTAGCCC-GGACCTCACCCCATGCTGTGCAACTGGGGGTTCAGGC 908
Query  953  TGTGGTCTACCACGGGGCTATCTTCCCTTTCGGGACCCCAAC-AGCGAGGAGAACAGCA 1011
Sbjct  909  TGTGATCTATCATGGGGCTACCTTCCCTTTCGAGACCCTA-CTATTGACGAAAACAGCA 967
Query  1012  ACGATATTGCCCTGGTCCACCTCTCCAG-TCCCCTGCCCTCAGAGATACATCCAGCCT 1070
Sbjct  968  ATGACATTGCTTGGTCCACCTCTCTAGCTCCC-TGCCTCTCAGAGATACATCCAGCCA 1026
Query  1071  GTGTGCCTCCCAGCTGCCGGCCAGGCCCTGGTGGATGGCAAGATCTGTACCGTGACGGGC 1130
Sbjct  1027  GTGTGTCTCCCTGCTGCGGGACAGGCCCTGGTGGATGGCAAGGTCTGTACTGTGACCGGC 1086
Query  1131  TGGGGCAACACGAGTACTATGGCCAACAGGCCGGGTACTCCAGGAGGCTCGAGTCCCC 1190
Sbjct  1087  TGGGGTAACACACAGTTCTATGGCCAACAGGCTATGGTGTCTCAAGAGGCCGGGTTCCT 1146
Query  1191  ATAATCAGCAATGATGTCTGCAATGGCGCTGACTTCTATGGAAACAGATCAAGCCCAAG 1250
Sbjct  1147  ATCATAAGCAACGAAGTTTGCAACAGCCCCGACTTCTACGGGAATCAGATCAAGCCCAAG 1206
Query  1251  ATGTTCTGTGCTGGCTACCCGAGGGTGGCATTGATGCCTGCCAGGGCGACAGCGGTGGT 1310
Sbjct  1207  ATGTTCTGTGCTGGCTATCCTGAGGGTGGCATTGATGCGTGCCAGGGCGACAGTGGAGGC 1266
Query  1311  CCCTTTGTGTGTGAGGACAGCATCTCTCGGACGCCACGTTGGCGGCTGTGTGGCATTGTG 1370
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Sbjct  1387  TTCCGGGAGTGGATCTTCAAGGCCATAAAGACTCACTCCGAAGCCAGTGGCATGGTGACT 1446
Query  1491  CAGCTCTGA-CCGG--TGG-CT---T-CTC-G---CTGCGC-AGCCTCCAGGGCCCGAG-- 1536
Sbjct  1447  CAGCCCTGATCCGCGCTCATCTCGCTGCTCCGTGCTGCACTAGCATCCAGAGTCAGAGTT 1506
Query  1537  G-T--GAT--C-CC-G-----GTGGTGGGATCCACGCTGGGCGG-AGGATGGGACGTTT 1582
Sbjct  1507  GGTCTGGTGGCTCCAGCCCCACGTGGTAGGCTCCACACTGGGCCTCAC-ATGGAATGGTT 1565
Query  1583  TTCTTCTTGGGCCCCGTCCACAGGTCCAAGGACACCCCTCCCTCCAGGGTCTCTCTTCCA 1642
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Query 1643  CAGTGGCGGGCCCACTCAGCCCC-GAGACCACCCAACTCACCTCCTGACCCCCATGTA 1701
Sbjct 1624  CAGTGGCGGGCCCACTCAATCCCAGGG-CCATTGG-CCTCACCTCCC-ACCCC-ATGTA 1679

Query 1702  AATATTGTTCTG-CTGTCTGGGACTC-CTGTCTAGGT-GCCCCGTATGATGG-GATGCTC 1757
Sbjct 1680  AATATTACTCTGTCC-TCTGGGGGCGCT--CTAGGGAGCCCCCT--TG-TGCAGATGCTC 1733

Query 1758  TTTAAATAATAAAGATGGTTTTGATT 1783
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>ref|NM_001110252.1|  Mus musculus hepsin (Hpn), transcript variant 1, mRNA
Length=1830

GENE ID: 15451 Hpn | hepsin [Mus musculus] (Over 10 PubMed links)

Score = 1245 bits (674), Expect = 0.0
Identities = 1282/1569 (81%), Gaps = 68/1569 (4%)
Strand=Plus/Plus

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Query 259  AGGGTGGCCGGA CTG-TGCCATGCTGCTCCAGACCCAAGGTGGCAGCTCTCACTGCGGGG 317
Sbjct 280  AGGGTGGCCGGA CTGAG-CATGCTGCTCCAGACCCAAGGTGGCAGCTCTCATTGTGGGT 338

Query 318  ACCCTGCTACTTC-TGACAGCCATCGGGGCGGCATCCTGGGCCATTGTGGCTGTTCTCCT 376
Sbjct 339  ACCCTGCTG-TTCCTGACAGGCA TTGGGGCCGCTCCTGGGCCATTGTGACCATCCTACT 397

Query 377  -CAGGAGTGACCAAGGAGCCGCTGTACCCAGTGCAGGTGAGCTCT-GCGGACGCTCGGCTC 434
Sbjct 398  GCAG-AGTGACCAAGGAGCCACTGTACCAAGTGCAGCTCAG-TCCAGGGGACTCACGGCTT 455

Query 435  ATGGTCTTTGACAAGACGGAAGGGA-CGTGGCGGCTGCTGTGCTCCTCGCGCTCCAACGC 493
Sbjct 456  GCGGTGTTTGAACAAGACGGA-GGGAACGTGGAGGCTACTGTGCTCCTCACGCTCCAATGC 514

Query 494  CAGGGTAGCCGGA CTGAGTGCAGGAGATGGGCTTCTCAGGGCACTGACCCACTCCGA 553
Sbjct 515  CAGGGTGGCAGGGCTCGGCTGTGAGGAGATGGGCTTCTCAGGGCTCTGGCGCACTCGGA 574

Query 554  GCTGGACGTGCGAA CGGCGGGCGCCAATGGCACGTCGGGCTTCTTCTGTGTGGACAGGG 613
Sbjct 575  GCTGGATGTGCGCA CTGCGGGCGCCAACGGCACATCGGGCTTCTTTTTCGTGGACAGGG 634

Query 614  GAGG-CTGCCCCACACCCAGAGGCTGCTGGAGGTCACTCCGTGTGTGATTGCCCCAGAG 672
Sbjct 635  C-GGACTGCCCTCTGGCTCAGAGGTTGCTGGATGTCACTCTGTATGTGACTGTCTAGAG 693

Query 673  GCCGTTTCTTGGCCGCCATCTGCCAAGACTGTGGCCGAGGAAGCTGCCCGTGGACCGCA 732
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Query 733  TCGTGGGAGGCCGGGACACCCAG-CTTGGGCGGTGGCCGTGGCAAGTCAGCCTTCGCTAT 791
Sbjct 754  TTGTGGGGGGCCAGGACAGCAGTCT-GGGAAGGTGGCCGTGGCAGGTGAGCCTGCGTTAT 812

Query 792  GATGG-AGCACACCTCTGTGGGGGATCCCTGCTCTCCGGGGA CTGGGTGCTGACAGCCGC 850
Sbjct 813  GATGGGACC-CACCTCTGTGGGGGTCCCTGCTGTCTGGGGA CTGGGTGCTGACTGCTGC 871

Query 851  CCACTGCTTCCCGAGCGGAACCGGGTCTGTCCCGATGGCGAGTGTGTCGGGTGCCGT 910
Sbjct 872  ACATTGCTTTCCAGAGCGGAACCGGGTCTGTCTCGGTGGCGAGTATTGCTGGTGTCTGT 931

Query 911  GGCCCAGG-CCTCTCCCAACGCTCTGCAGCTGGGGGTGCAGGCTGTGGTCTACCAAGGG 969
Sbjct 932  AGCCC-GGACCTCACCCCATGCTGTGCAACTGGGGGTT CAGGCTGTGATCTATCATGGGG 990

Query 970  GCTATCTTCCCTTTTCGGGACCCCAAC-AGCGAGGAGAACAGCAACGATATTGCCCTGGTC 1028
Sbjct 991  GCTACCTTCCCTTTTCGAGACCCTA-CTATCGACGAAAACAGCAATGACATTGCCTTGGTC 1049

Query 1029  CACCTCTCCAG-TCCCCTGCCCTCACAGAATACATCCAGCCTGTGTGCTCCAGCTGC 1087
Sbjct 1050  CACCTCTCTAGCTCCC-TGCCTCTCACAGAATACATCCAGCCAGTGTGTCTCCCTGCTGC 1108

Query 1088  CGGCCAGGCCCTTGGTGGATGGCAAGATCTGTACCGTGACGGGCTGGGGCAACACGAGTA 1147
Sbjct 1109  GGGACAGGCCCTTGGTGGATGGCAAGGTCTGTACTGTGACCGGCTGGGGTAACACAGTT 1168

Query 1148  CTATGGCCAAACAGGCCGGGTACTCCAGGAGGCTCGAGTCCCCATAATCAGCAATGATGT 1207
Sbjct 1169  CTATGGCCAAACAGGCTATGGTGCTCCAAGAGGCCCGGGTTC CATATAAGCAACGAAGT 1228

Query 1208  CTGCAATGGCGCTGACTTCTATGGAAACCAGATCAAGCCCAAGATGTTCTGTGCTGGCTA 1267
Sbjct 1229  TTGCAACAGCCCCGACTTCTACGGGAATCAGATCAAGCCCAAGATGTTCTGTGCTGGCTA 1288

Query 1268  CCCCAGGGGTGGCATTGATGCTGCCAGGGCGACAGCGGTGGTCCCTTTGTGTGTGAGGA 1327
Sbjct 1289  TCCTGAGGGTGGCATTGATGCTGCCAGGGCGACAGTGGAGGCCCTTTGTGTGTGAAGA 1348

Query 1328  CAGCATCTCTCGGACGCCACGTTGGCGGCTGTGTGGCATTGTGAGTTGGGGCACTGGCTG 1387

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Sbjct  1349  CAGCATCTCTGGGACATCAAGGTGGCGGCTATGTGGCATTGTAAGCTGGGGTACGGGCTG 1408
Query  1388  TGCCCTGGCCCAAGCCAGGCGTCTACACCAAAGTCAGTGACTTCGGGAGTGATCTT 1447
Sbjct  1409  TGCTTTGGCCCGGAAGCCAGGAGTGTACACCAAAGTCACTGACTTCGGGAGTGATCTT 1468
Query  1448  CCAGGCCATAAAGACTCACTCCGAAGCCAGCGGCATGGTGACCCAGCTCTGA-CCGG--T 1504
Sbjct  1469  CAAGGCCATAAAGACTCACTCCGAAGCCAGTGGCATGGTGACTCAGCCCTGATCCCGCCT 1528
Query  1505  GG-CT---T-CTC-G--CTGCGC-AGCCTCCAGGGCCCGAG--G-T--GAT--C-CC-G- 1545
Sbjct  1529  CATCTCGCTGCTCCGTGCTGCACTAGCATCCAGAGTCAGAGTTGGTCTGGTGGCTCCAGC 1588
Query  1546  -----GTGGTGGGATCCACGCTGGGCGG-AGGATGGGACGTTTTTCTTCTTGGGCCCGGT 1599
Sbjct  1589  CCCACGTGGTAGGCTCCACACTGGGCCTCAC-ATGGAATGGTTTCTGCTCAGATCCAGT 1647
Query  1600  CCACAGGTCCAAGGACACCCCTCCCTCCAGGGTCTCTCTTCCACAGTGGCGGGCCCACTC 1659
Sbjct  1648  CCACGGGTCCAAGGATGC--TGGATCCAAGGACTTCTCTTCCACAGTGGCCGGCCCACTC 1705
Query  1660  AGCCCC-GAGACCACCAACCTCACCTCTGACCCCCATGTAAATATTGTTCTG-CTGT 1717
Sbjct  1706  AATCCAGGG-CCATTGG-CCTCACCTCCC-ACCCC-ATGTAAATATTACTCTGTCC-T 1760
Query  1718  CTGGGACTC-CTGTCTAGGT-GCCCCGTGATGATGG-GATGCTCTTTAAATAATAAAGATG 1774
Sbjct  1761  CTGGGGGCGCT--CTAGGGAGCCCT--TG-TGAGATGCTCTTTAAATAATAAAGGTG 1815
Query  1775  GTTTTGATT 1783
Sbjct  1816  GTTTTGATT 1824

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>gb|BC138809.1| Mus musculus hepsin, mRNA (cDNA clone MGC:170436 IMAGE:8861831), complete cds
Length=1505

Score = 1240 bits (671), Expect = 0.0
Identities = 1075/1271 (84%), Gaps = 23/1271 (1%)
Strand=Plus/Plus

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Query  259  AGGGTGGCCGGA CTG-TGCCATGCTGCTCCAGACCCAAGGTGGCAGCTCTCACTGCGGGG 317
Sbjct  160  AGGGTGGCCGGA CTGAG-CATGCTGCTCCAGACCCAAGGTGGCAGCTCTCATTGTGGGT 218
Query  318  ACCCTGCTACTTC-TGACAGCCATCGGGGCGGCATCCTGGGCCATTGTGGCTGTTCTCCT 376
Sbjct  219  ACCCTGCTG-TTCCTGACAGGCATTGGGGCCGCGTCTCTGGGCCATTGTGACCATCCTACT 277
Query  377  -CAGGAGTGACCAAGGAGCCGCTGTATCCCAAGTGCAGGTGAGCTCT-GCGGACGCTCGGCTC 434
Sbjct  278  GCAG-AGTGACCAAGGAGCCACTGTACCAAGTGCAGCTCAG-TCCAGGGGACTCACGGCTT 335
Query  435  ATGGTCTTTTGACAAGACGGAAGGGA-CGTGGCGGCTGCTGTGCTCCTCGCGCTCCAACGC 493
Sbjct  336  GCGGTGTTTGACAAGACGGA-GGGAACGTGGAGGCTACTGTGCTCCTCACGCTCCAATGC 394
Query  494  CAGGGTAGCCGGACTCAGCTGCGAGGAGATGGGCTTCTCAGGGCACTGACCCACTCCGA 553
Sbjct  395  CAGGGTGGCAGGGCTCGGCTGTGAGGAGATGGGCTTTCTCAGGGCTCTGGCGCACTCGGA 454
Query  554  GCTGGACGTGCGAACGGCGGGCGCCAATGGCACGTCGGGCTTCTTCTGTGTGGACGAGGG 613
Sbjct  455  GCTGGATGTGCGCACTGCGGGCGCCAACGGCACATCGGGCTTCTTTTTCGTGGACGAGGG 514
Query  614  GAGG-CTGCCCCACCCAGAGGCTGCTGGAGGTATCTCCGTGTGTGATTGCCCCAGAG 672
Sbjct  515  C-GGACTGCCTCTGGCTCAGAGGTGCTGGATGTATCTCTGTATGTGACTGTCTTAGAG 573
Query  673  GCCGTTTCTTGGCCGCCATCTGCCAAGACTGTGGCCGAGGAAGCTGCCCGTGGACCGCA 732
Sbjct  574  GCCGATTCTTGA CTGCCACCTGCCAAGACTGTGGCCGAGGAAGCTGCCCGTGGACCGCA 633
Query  733  TCGTGGGAGGCCGGGACACCAG-CTTGGGCGGGTGGCCGTGGCAAGTCAGCCTTCGCTAT 791
Sbjct  634  TTGTGGGGGGCCAGGACAGCAGTCT-GGGAAGGTGGCCGTGGCAGGTGAGCCTGCGTTAT 692
Query  792  GATGG-AGCACACTCTGTGGGGGATCCCTGCTCTCCGGGACTGGGTGCTGACAGCCGC 850
Sbjct  693  GATGGGACC-CACCTCTGTGGGGGTCCCTGCTGTCTGGGGACTGGGTGCTGACTGCTGC 751
Query  851  CCACTGCTTCCCGGAGCGGAACCGGGTCTGTCCCGATGGCGAGTGTGTCGGGTGCCGT 910
Sbjct  752  ACATTGCTTTCCAGAGCGGAACCGGGTCTGTCTCGGTGGCAGTATTTGCTGGTGTGT 811
Query  911  GGCCCAAG-CTTCTCCACCGGTCTGCAGCTGGGGGTGCAGGCTGTGGTCTACACGGGG 969
Sbjct  812  AGCCC-GGACCTCACCCATGCTGTGCAACTGGGGGTTAGGCTGTGATCTATCATGGGG 870
Query  970  GCTATCTTCCCTTTTCGGGACCCCAAC-AGCGAGGAGAACAGCAACGATATTGCCCTGGTC 1028
Sbjct  871  GCTACCTTCCCTTTTCGAGACCCTA-CTATCGACGAAAACAGCAATGACATTGCCTTGGTC 929
Query  1029  CACCTCTCCAG-TCCCTGCCCTCACAGAATACATCCAGCCTGTGTGCTCTCCAGCTGC 1087
Sbjct  930  CACCTCTCTAGCTCCC-TGCCTCTCACAGAATACATCCAGCCAGTGTGTCTCCCTGCTGC 988

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Query 1088 CGGCCAGGCCCTGGTGGATGGCAAGATCTGTACCGTGACGGGCTGGGGCAACACGAGTA 1147
          |||
Sbjct 989 GGGACAGGCCCTGGTGGATGGCAAGGTCTGTACTGTGACCGGCTGGGGTAACACACAGTT 1048

Query 1148 CTATGGCCAAACAGGCCGGGTACTCCAGGAGGCTCGAGTCCCCATAATCAGCAATGATGT 1207
          |||
Sbjct 1049 CTATGGCCAAACAGGCTATGGTGCTCCAAAGAGGCCGGGTTCCTATCATAAGCAACGAAGT 1108

Query 1208 CTGCAATGGCGCTGACTTCTATGGAAACCAGATCAAGCCCAAGATGTTCTGTGCTGGCTA 1267
          |||
Sbjct 1109 TTGCAACAGCCCCGACTTCTACGGGAATCAGATCAAGCCCAAGATGTTCTGTGCTGGCTA 1168

Query 1268 CCCCAGGGGTGGCATTGATGCGTGCAGGGCGACAGCGGTGGTCCCTTTGTGTGTGAGGA 1327
          |||
Sbjct 1169 TCCTGAGGGTGGCATTGATGCGTGCAGGGCGACAGTGGAGGCCCTTTGTGTGTGAAGA 1228


Query 1328 CAGCATCTCTCGGACGCCACGTTGGCGGCTGTGTGGCATTGTGAGTTGGGGCACTGGCTG 1387
          |||
Sbjct 1229 CAGCATCTCTGGGACATCAAGTGGCGGCTATGTGGCATTGTAAGCTGGGGTACGGGCTG 1288

Query 1388 TGCCCTGGCCCAAGCCAGGCGTCTACACCAAAGTCAGTGACTTCCGGGAGTGGATCTT 1447
          |||
Sbjct 1289 TGCTTTGGCCCGGAAGCCAGGAGTGTACACCAAAGTCACTGACTTCCGGGAGTGGATCTT 1348

Query 1448 CCAGGCCATAAAGACTCACTCCGAAGCCAGCGGCATGGTGACCCAGCTCTGA-CCGGTGG 1506
          |||
Sbjct 1349 CAAGGCCATAAAGACTCACTCCGAAGCCAGTGGCATGGTGACTCAGCCCTGATCCCGCCT 1408

Query 1507 CTTCTCGCTGC 1517
          |||
Sbjct 1409 CATCTCGCTGC 1419

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>dbj|AK156553.1|  Mus musculus activated spleen cDNA, RIKEN full-length enriched library, clone:F830029I12 product:hepsin, full insert sequence
Length=1745

GENE ID: 15451 Hpn | hepsin [Mus musculus] (Over 10 PubMed links)

Score = 1240 bits (671), Expect = 0.0
Identities = 1282/1570 (81%), Gaps = 70/1570 (4%)
Strand=Plus/Plus

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Query 259 AGGGTGGCCGACTG-TGCCATGCTGCTCCAGACCCAAAGGTGGCAGCTCTCACTGCGGGG 317
          |||
Sbjct 195 AGGGTGGCCGACTGCAG-CATGCTGCTCCAGACCCAAAGGTGGCAGCTCTCATTGTGGGT 253

Query 318 ACCCTGCTACTTC-TGACAGCCATCGGGCGGCATCCTGGGCCATTGTGGCTGTTCTCCT 376
          |||
Sbjct 254 ACCCTGCTG-TTCCTGACAGGCATTGGGGCCGCTCCTGGGCCATTGTGACCATCCTACT 312

Query 377 -CAGGAGTGACAGGAGCCGCTGTATCCCAAGTGCAGG-TCAGCTCT-GCGGACGCTCGGCT 433
          |||
Sbjct 313 GCAG-AGTGACAGGAGCCACTGTATCCAAAGTGC-GGCTCAG-TCCAGGGGACTCACGGCT 369

Query 434 CATGGTCTTTGACAAGACGGAAGGGA-CGTGGCGGCTGCTGTGCTCCTCGCGCTCCAACG 492
          |||
Sbjct 370 TGCGGTGTTTGACAAGACGGA-GGGAACGTGGAGGCTACTGTGCTCCTCACGCTCCAATG 428

Query 493 CCAGGGTAGCCGGAAGTCACTGCTGCGAGGAGATGGGCTTCTCAGGGCACTGACCCACTCCG 552
          |||
Sbjct 429 CCAGGGTGGCAGGGCTCGGCTGTGAGGAGATGGGCTTTCTCAGGGCTCTGGCACACTCGG 488

Query 553 AGCTGGACGTGCGAACGGCGGGCGCCAATGGCAGTCGGGCTTCTTCTGTGTGGACGAGG 612
          |||
Sbjct 489 AGCTGGATGTGCGCACTGCGGGCGCCAACGGCAGTCGGGCTTCTTTTGCCTGGACGAGG 548

Query 613 GGAGG-CTGCCCCACACCCAGAGGCTGCTGGAGGTCTATCTCCGTGTGTGATTGCCCCAGA 671
          |||
Sbjct 549 GC-GGACTGCGCTCTGGCTCAGAGGTGTGCTGGATGTCATCTCTGTATGTGACTGTCTAGA 607

Query 672 GGCCGTTTCTTGGCCGCCATCTGCCAAGACTGTGGCCGCAGGAAGCTGCCCCGTGGACCGC 731
          |||
Sbjct 608 GGCCGATTCTTACTGCTGACCACTGCCAAGACTGTGGCCGCAGGAAGCTGCCGGTGGACCGC 667

Query 732 ATCGTGGGAGGCCGGGACACCAG-CTTGGGCCGGTGGCCGTGGCAAGTCAGCCTTCGCTA 790
          |||
Sbjct 668 ATTTGCGGGGGCCAGGACAGCAGTCT-GGGAAGGTGGCCGTGGCAGGTGAGCCTGCGTTA 726

Query 791 TGATGG-AGCACACCTCTGTGGGGGATCCCTGCTCTCCGGGACTGGGTGCTGACAGCCG 849
          |||
Sbjct 727 TGATGGGA-CTCACCTCTGTGGGGGTCCCTGCTGTCTGGGGACTGGGTGCTGACTGCTG 785

Query 850 CCCACTGCTTCCCGGAGCGGAACCGGGTCTGTCCCGATGGCGAGTGTGTCGGTGCCG 909
          |||
Sbjct 786 CACATTGCTTTCCAGAGCGGAACCGGGTCTGTCTCGGTGGCGAGTATTTGCTGGTGCTG 845

Query 910 TGGCCCAGG-CCTCTCCCCACGGTCTGCAGCTGGGGGTGCAGGCTGTGGTCTACCACGGG 968
          |||
Sbjct 846 TAGCCC-GGACCTACCCCATGCTGTGCAACTGGGGGTTCAGGCTGTGATCTATCATGGG 904

Query 969 GGCTATCTTCCCTTTTCGGGACCCCAAC-AGCGAGGAGAACAGCAACGATATTGCCCTGGT 1027
          |||
Sbjct 905 GGCTACCTTCCCTTTTCGAGACCCCTA-CTATCGACGAAAACAGCAATGACATTGCCCTGGT 963


Query 1028 CCACCTCTCCAG-TCCCCTGCCCTCACAGAATACATCCAGCCTGTGTGCCTCCAGCTG 1086
          |||

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Sbjct  964      |||CTCTCTAGCTCCC-TGCCTCTCACAGAATACATCCAGCCAGTGTGTCTCCCTGCTG      1022
Query  1087    CCGGCCAGGCCCTGGTGGATGGCAAGATCTGTACCGTGACGGGCTGGGGCAACACGCAGT      1146
Sbjct  1023    CGGGACAGGCCCTGGTGGATGGCAAGGTCTGTACTGTGACCGGCTGGGGTAACACACAGT      1082
Query  1147    ACTATGGCCAACAGGCCGGGTACTCCAGGAGGCTCGAGTCCCCATAATCAGCAATGATG      1206
Sbjct  1083    TCTATGGCCAACAGGCTATGGTGCTCCAAGAGGCCCGGTTCCCATCATAAGCAACGAAG      1142
Query  1207    TCTGCAATGGCGCTGACTTCTATGGAAACAGATCAAGCCCAAGATGTTCTGTGCTGGCT      1266
Sbjct  1143    TTTGCAACAGCCCCGACTTCTACGGGAATCAGATCAAGCCCAAGATGTTCTGTGCTGGCT      1202
Query  1267    ACCCCGAGGGTGGCATTGATGCCTGCCAGGGCGACAGCGGTGGTCCCTTTGTGTGTGAGG      1326
Sbjct  1203    ATCTGTAGGGTGGCATTGATGCGTGCCAGGGCGACAGTGGAGGCCCTTTGTGTGTGAAG      1262
Query  1327    ACAGCATCTCTCGGACGCCAGTTGGCGGCTGTGTGGCATTGTGAGTTGGGGCACTGGCT      1386
Sbjct  1263    ACAGCATCTCTGGGACATCAAGGTGGCGGCTATGTGGCATTGTAAGCTGGGGTACGGGCT      1322
Query  1387    GTGCCCTGGCCAGAACGCCAGGCGTCTACACCAAAGTCAGTGACTTCCGGGAGTGGATCT      1446
Sbjct  1323    GTGCTTTGGCCCGGAAGCCAGGAGTGACACCAAAGTCACTGACTTCCGGGAGTGGATCT      1382
Query  1447    TCCAGGCCATAAAGACTCACTCCGAAGCCAGCGGCATGGTGACCCAGCTCTGA-CCGG--      1503
Sbjct  1383    TCAAGGCCATAAAGACTCACTCCGAAGCCAGTGGCATGGTGACTCAGCCCTGATCCCGCC      1442
Query  1504    TGG-CT---T-CTC-G--CTGCGC-AGCCTCCAGGGCCCGAG--G-T--GAT--C-CC-G      1545
Sbjct  1443    TCATCTCGCTGCTCCGTGCTGCACTAGCATCCAGAGTCAGAGTTGGTCTGGTGGCTCCAG      1502
Query  1546    -----GTGGTGGGATCCACGCTGGGCCG-AGGATGGGACGTTTTTCTTCTTGGGCCCGG      1598
Sbjct  1503    CCCACGTGGTAGGCTCCACACTGGGCCTCAC-ATGGAATGGTTTCCTGCTCAGATCCAG      1561
Query  1599    TCCACAGGTCCAAGGACACCCTCCCTCCAGGGTCTCTCTTCCACAGTGGCGGGCCCACT      1658
Sbjct  1562    TCCACGGGTCCAAGGATGC--TGGATCCAAGGACTTCTCTTCCACAGTGGCCGGCCCACT      1619
Query  1659    CAGCCCC-GAGACCACCCAACCTCACCCCTCCTGACCCCATGTAAATATTGTTCTG-CTG      1716
Sbjct  1620    CAATCCACAGGG-CCATTGG-CCTCACCTCCC-ACCCC-ATGTAATATTACTCTGTCC-      1674
Query  1717    TCTGGGACTC-CTGTCTAGGT-GCCCTGATGATGG-GATGCTCTTTAAATAATAAAGAT      1773
Sbjct  1675    TCTGGGGGGCGCT--CTAGGGAGCCCT--TG-TGCAGATGCTCTTTAAATAATAAAGGT      1729
Query  1774    GGTTTTGATT      1783
Sbjct  1730    GGTTTTGATT      1739

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>dbj|AK002694.1|  Mus musculus adult male kidney cDNA, RIKEN full-length enriched library, clone:0610030A17 product:hepsin, full insert sequence
Length=1814

GENE ID: 15451 Hpn | hepsin [Mus musculus] (Over 10 PubMed links)

Score = 1181 bits (639), Expect = 0.0
Identities = 1275/1573 (81%), Gaps = 80/1573 (5%)
Strand=Plus/Plus

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Query  259    AGGGTGGCCGGA CTG-TGCCATGCTGCTCCAGACCCAAGGTGGCAGCTCTCACTGCGGGG      317
Sbjct  274    AGGGTGGCCGGA CTGAG-CATGCTGCTCCAGACCCAAGGTGGCAGCTCTCATTGTGGGT      332
Query  318    ACCCTGCTACTT-CTGACAGCCATCGGGGCGGCATCCTGGGCCATTGTGGCTGTTCTCCT      376
Sbjct  333    ACCCTGCT-GTTCCTGACAGGCATTGGGGCCGCGTCCTGGGCCATTGTGACCATCTTACT      391
Query  377    -CAGGAGTGACCAGGAGCCGCTGTACCCAGTGCAAGTCAGCT-CTGCGGACGCTCGGCTC      434
Sbjct  392    GCA-GAGTGACCAGGAGCCACTGTACCAAGTGCAAGTCAGCTCAG-TCCAGGGGACTCACGGCTT      449
Query  435    ATGGTCTTTTGACAAGACGGAAGGG-ACGTGGCGGCTGCTGTGCTCCTCGCGCTCCAACGC      493
Sbjct  450    GCGGTGTTTGTACAAGACGG-AGGGAACGTGGAGGCTACTGTGCTCCTCACGCTCCAATGC      508
Query  494    CAGGGTAGCCGGACTCAGCTGCGAGGAGATGGGCTTCTCAGGGCACTGACCCACTCCGA      553
Sbjct  509    CAGGGTGGCAGGGCTCGGCTGTGAGGAGATGGGCTTCTCAGGGCTCTGGCGCACTCGGA      568
Query  554    GCTGGACGTGCGAACGCGGGCGCCAAATGGCACGTCGGGCTTCTTCTGTGTGGACGAGGG      613
Sbjct  569    GCTGGATGTGCGCACTGCGGGCGCCAACGGCACATCGGGCTTCTTTTGCCTGGACGA-GG      627
Query  614    GAGG-CTGCCCCACACCAGAGGCTGCTGGAGGTCACTCCCGTGTGTGATTGCCCCAGAG      672
Sbjct  628    GCGGACTGCCTCTGGCTCAGAGGTTGCTGGATGTATCTCTGTATGTGACTGTCCTAGAG      687
Query  673    GCCGTTTCTTGGCCGCCATCTGCCAAGACTGTGGCCGCAGGAAGCTGCCCGTGGACCGCA      732
Sbjct  688    GCCGATTCTGACTGCCACCTGCCAAGACTGTGGCCGCA-GAAGCTGCCGGTGGACCGCA      746

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Query 733 TCGTGGGAGGCCGGGACACCAGCT-TGGGCGCGTGGCCGTGGCAAGTCAGCCTTCGCTAT 791
Sbjct 747 TTGTGGGGGGCCAGGACAGCAG-TCTGGGAAGGTGGCCGTGGCAGGTCAGCCTGCGTTAT 805

Query 792 GATGGAGCA-CACCTCTGTGGGGATCCCTGCTCTC-CGGGGACTGGGTGCTGACAGCCG 849
Sbjct 806 GATGG-GTACCACCTCTGTGGGGGT-CCTGCTGTCTC-GGGACTGGGTGCTGACTGCTG 862

Query 850 CCCACTGCTTCCCGGAGC-GGA-ACCGGGTCCTGTCCCGATGGCGAGTGTTCGCCGGTGC 907
Sbjct 863 CACATTGCTTTCAGAGCGGGAGA-C-GGTCTGTCTCGGTGGCGAGTATTGCTGGTGC 920

Query 908 CGTGGCCCAAG-CCTCTCCCCACGGTCTGCAGCTGGGGGTGCAGGCTGTGGTCTACCACG 966
Sbjct 921 TGTAGCCC-GGACCTCACCCCATGCTGTGCAACT-GGGGTTCAGGCTGTGATCTATCATG 978

Query 967 GGGGCTATCTTCC-CTTTCGGGACCCCAAC-AGCGAGGAGAACAGCAACGATATTGCCCT 1024
Sbjct 979 GGGGCTA-CCTCTCTTTTCGAGA-CCCTACTATCGACGAAAAACAGCAATGACATTGCCTT 1036

Query 1025 GGTCCACCTCTCCAGTC-CCCTGCCCTCACAGAATACATCCAGCCTGTGTGCCTCCAG 1083
Sbjct 1037 GGTCAACCTCTCTAG-CTCCCTGCCTCTCACAGAATACATCCAGCCAGTGTGTCTCCCTG 1095

Query 1084 CTGCCGGCCAGGCCCTGGTGGATGGCAAGATCTGTACCGTGACGGGCTGGGGCAACACGC 1143
Sbjct 1096 CTGCCGGACAGGCCCTGGTGGATGGCAAGGTCTGTACTGTGACCGGCTGGGGTAACACAC 1155

Query 1144 AGTACTATGGCCAAACAGGCCGGGTACTCCAGGAGGCTCGAGTCCCCATAATCAGCAATG 1203
Sbjct 1156 AGTTCTATGGCCAAACAGGCTATGGTCTCCAAGAGGCCCGGGTTCCCATCATAAGCAACG 1215

Query 1204 ATGTCTGCAATGGCGCTGACTTCTATGGAACAGATCAAGCCCAAGATGTTCTGTGCTG 1263
Sbjct 1216 AAGTTTGCAACAGCCCCGACTTCTACGGGAATCAGATCAAGCCCAAGATGTTCTGTGCTG 1275

Query 1264 GCTACCCCGAGGGTGGCATTGATGCCTGCCAGGGCGACAGCGGTGGTCCCTTTGTGTGTG 1323
Sbjct 1276 GCTATCCTGAGGGTGGCATTGATGCCTGCCAGGGCGACAGTGGAGGCCCTTTGTGTGTG 1335

Query 1324 AGGACAGCATCTCTCGACGCCACGTGGCGGCTGTGTGCATTGTGAGTTGGGGCACTG 1383
Sbjct 1336 AAGACAGCATCTCTGGACATCAAGGTGGCGGCTATGTGGCATTGTAAGCTGGGGTACGG 1395

Query 1384 GCTGTGCCCTGGCCAGAACCCAGGCGTCTACACCAAAGTCAGTGACTTCCGGGAGTGGA 1443
Sbjct 1396 GCTGTGCTTTGGCCCGAAGCCAGGAGGTACACCAAAGTCACTGACTTCCGGGAGTGGA 1455

Query 1444 TCTTCCAGGCCATAAAGACTCACTCCGAAGCCAGCGGCATGGTGACCCAGCTCTGA-CCG 1502
Sbjct 1456 TCTTCAAGGCCATAAAGACTCACTCCGAAGCCAGTGGCATGGTGACTCAGCCCTGATCCC 1515

Query 1503 G--TGG-CT---T-CTC-G--CTGCGC-AGCCTCCAGGGCCCCGAG--G-T--GAT--C-C 1543
Sbjct 1516 GCCTCATCTCGTGCTCCGTGCTGCACTAGCATCCAGAGTCAGAGTTGGTCTGGTGGCTC 1575

Query 1544 C-G-----GTGGTGGGATCCACGCTGGGCGG-AGGATGGGACGTTTTTCTTCTTGGGCC 1595
Sbjct 1576 CAGCCCCACGTGGTAGGCTCCACACTGGGCCTCAC-ATGGAATGGTTTCTGCTCAGATC 1634


Query 1596 CGGTCCACAGGTCCAAGGACACCCCTCCCTCCAGGGTCTCTCTTCCACAGTGGCGGGCCC 1655
Sbjct 1635 CAGTCCACGGGTCCAAGGATGC--TGGATCCAGGGACTTCTCTTCCACAGTGGCGGGCCC 1692

Query 1656 ACTCAGCCCC-GAGACCACCAACCTCACCTCCTGACCCCCATGTAATATTGTTCTG- 1713
Sbjct 1693 ACTCAATCCAGGG-CCATTGG-CCTCACCTCCC-ACCCC-ATGTAAATATTACTCTGT 1748

Query 1714 CTGTCTGGGACTC-CTGTCTAGGT-GCCCCGTGATGATGG-GATGCTCTTTAAATAATAAA 1770
Sbjct 1749 CC-TCTGGGGGGCGCT--CTAGGGAGCCCCCT--TG-TGAGATGCTCTTTAAATAATAAA 1802

Query 1771 GATGGTTTTGATT 1783
Sbjct 1803 GGTGGTTTT-ATT 1814

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>ref|XM_512584.2|  PREDICTED: Pan troglodytes hepsin (transmembrane protease, serine 1), transcript variant 3 (HPN), mRNA
Length=1572

GENE ID: 455944 HPN | hepsin (transmembrane protease, serine 1)
[Pan troglodytes]

Sort alignments for this subject sequence by:
E value Score Percent identity
Query start position Subject start position

Score = 1011 bits (547), Expect = 0.0
Identities = 549/550 (99%), Gaps = 0/550 (0%)
Strand=Plus/Plus

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Query 658 GTGATTGCCCCAGAGGCCGTTTCTTGGCCGCCATCTGCCAAGACTGTGGCCGAGGAAGC 717
Sbjct 490 GTGATTGCCCCAGAGGCCGTTTCTTGGCCGCCATCTGCCAAGACTGTGGCCGAGGAAGC 549

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Query 718 TGCCCGTGGACCGCATCGTGGGAGGCCGGGACACAGCTTGGGCCGGTGGCCGTGGCAAG 777
Sbjct 550 TGCCCGTGGACCGCATCGTGGGAGGCCGGGACACAGCTTGGGCCGGTGGCCGTGGCAAG 609
Query 778 TCAGCCTTCGCTATGATGGAGCACACCTCTGTGGGGGATCCCTGCTCTCCGGGGACTGGG 837
Sbjct 610 TCAGCCTTCGCTATGATGGAGCACACCTCTGTGGGGGATCCCTGCTCTCCGGGGACTGGG 669
Query 838 TGCTGACAGCCGCCCAGTCTTCCCGAGCGGAACCGGGTCTGTCCCGATGGCGAGTGT 897
Sbjct 670 TGCTGACAGCCGCCCAGTCTTCCCGAGCGGAACCGGGTCTGTCCCGATGGCGAGTGT 729
Query 898 TTGCCGGTGGCCGTGGCCAGGCGCTCTCCCCACGGTCTGCAGCTGGGGGTGCAGGCTGTGG 957
Sbjct 730 TTGCCGGTGGCCGTGGCCAGGCGCTCTCCCCACGGTCTGCAGCTGGGGGTGCAGGCTGTGG 789
Query 958 TCTACCACGGGGGCTATCTTCCCTTTCGGGACCCCAACAGCGAGGAGAACAGCAACGATA 1017
Sbjct 790 TCTACCACGGGGGCTATCTTCCCTTTCGGGACCCCAACAGCGAGGAGAACAGCAACGATA 849
Query 1018 TTGCCCTTGGTCCACCTCTCCAGTCCCTGCCCTCACAGAATACATCCAGCCTGTGTGCC 1077
Sbjct 850 TTGCCCTTGGTCCACCTCTCCAGTCCCTGCCCTCACAGAATACATCCAGCCTGTGTGCC 909
Query 1078 TCCAGCTGCGCGCCAGGCCCTGGTGGATGGCAAGATCTGTACCGTGACGGGCTGGGGCA 1137
Sbjct 910 TCCAGCTGCGCGCCAGGCCCTGGTGGATGGCAAGATCTGTACCGTGACGGGCTGGGGCA 969
Query 1138 ACACGCAGTACTATGGCCAAACAGGCCGGGGTACTCCAGGAGGCTCGAGTCCCCATAATCA 1197
Sbjct 970 ACACGCAGTACTATGGCCAAACAGGCCGGGGTACTCCAGGAGGCTCGAGTCCCCATAATCA 1029
Query 1198 GCAATGATGT 1207
Sbjct 1030 GCAATGATGT 1039
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Score = 968 bits (524), Expect = 0.0
Identities = 528/530 (99%), Gaps = 0/530 (0%)
Strand=Plus/Plus

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Query 1254 TTCTGTGTGGTACTCCCGAGGGTGGCATTGATGCCTGCCAGGGCGACAGCGGTGGTCCC 1313
Sbjct 1041 TTCTGTGTGGTACTCCCGAGGGTGGCATTGATGCCTGCCAGGGCGACAGCGGTGGTCCC 1100
Query 1314 TTTGTGTGTGAGGACAGCATCTCTCGGACGCCACGTTGGCGGCTGTGTGGCATTGTGAGT 1373
Sbjct 1101 TTTGTGTGTGAGGACAGCATCTCTCGGACGCCACGTTGGCGGCTGTGTGGCATTGTGAGT 1160
Query 1374 TGGGGCACTGGCTGTGCCCTGGCCAGAAAGCCAGGCGTCTACACCAAAGTCAGTGACTTC 1433
Sbjct 1161 TGGGGCACTGGCTGTGCCCTGGCCAGAAAGCCAGGCGTCTACACCAAAGTCAGTGACTTC 1220
Query 1434 CGGGAGTGGATCTTCCAGGCCATAAAGACTCACTCCGAAGCCAGCGGCATGGTGACCCAG 1493
Sbjct 1221 CGGGAGTGGATCTTCCAGGCCATAAAGACTCACTCCGAAGCCAGCGGCATGGTGACCCAG 1280
Query 1494 CTCTGACCGGTGGCTTCTCGCTGCGCAGCCTCCAGGGCCCCAGGTGATCCCGGTGGTGGG 1553
Sbjct 1281 CTCTGACCGGTGGCTTCTCGCTGCGCAGCCTCCAGGGCCCCAGGTGATCCCGGTGGTGGG 1340
Query 1554 ATCCACGCTGGGCCGAGGATGGGACGTTTTTCTTCTTGGGCCCGGTCCACAGGTCCAAGG 1613
Sbjct 1341 ATCCACGCTGGGCCCTAGGATGGGACGTTTTTCTTCTTGGGCCCGGTCCACAGGTCCAAGG 1400
Query 1614 ACACCCCTCCCTCCAGGGTCTCTCTTCCACAGTGGCGGGCCCACTCAGCCCCGAGACCAC 1673
Sbjct 1401 ACACCCCTCCCTCCAGGGTCTCTCTTCCACAGTGGCGGGCCCACTCAGCCCCGAGACCAC 1460
Query 1674 CCAACCTCACCTCCTGACCCCATGTAAATATTGTTCTGCTGTCTGGGACTCCTGTCTA 1733
Sbjct 1461 CCAACCTCACCTCCTGACCCCATGTAAATATTGTTCTGCTGTCTGGGACTCCTGTCTA 1520
Query 1734 GGTGCCCTGATGATGGGATGCTCTTTAAATAATAAAGATGGTTTTGATT 1783
Sbjct 1521 GGTGCCCTGATGACGGGATGCTCTTTAAATAATAAAGATGGTTTTGATT 1570
```

Score = 638 bits (345), Expect = 3e-179
Identities = 345/345 (100%), Gaps = 0/345 (0%)
Strand=Plus/Plus


```
Query 191 GGTCCCACCTTGGCCAGGAGTCCAGCCAGGGAATCATTAAACAAGAGGCAGTGACATGGC 250
Sbjct 146 GGTCCCACCTTGGCCAGGAGTCCAGCCAGGGAATCATTAAACAAGAGGCAGTGACATGGC 205
Query 251 GCAGAAGGAGGGTGGCCGACTGTGCCATGTGCTCCAGACCCAAGGTGGCAGCTCTCAC 310
Sbjct 206 GCAGAAGGAGGGTGGCCGACTGTGCCATGTGCTCCAGACCCAAGGTGGCAGCTCTCAC 265
Query 311 TCGGGGACCCCTGCTACTTCTGACAGCCATCGGGGCGGCATCCTGGGCCATTGTGGCTGT 370
Sbjct 266 TCGGGGACCCCTGCTACTTCTGACAGCCATCGGGGCGGCATCCTGGGCCATTGTGGCTGT 325
Query 371 TCTCCTCAGGAGTGACAGGAGCCGCTGTACCCAGTGCAGGTGAGCTCTGCGGACGCTCG 430
Sbjct 326 TCTCCTCAGGAGTGACAGGAGCCGCTGTACCCAGTGCAGGTGAGCTCTGCGGACGCTCG 385
```

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Query  431  GCTCATGGTCTTTGACAAGACGGAAGGGACGTGGCGGCTGCTGTGCTCCTCGCGCTCCAA 490
Sbjct  386  GCTCATGGTCTTTGACAAGACGGAAGGGACGTGGCGGCTGCTGTGCTCCTCGCGCTCCAA 445

Query  491  CGCCAGGGTAGCCGGACTCAGCTGCGAGGAGATGGGCTTCCTCAG 535
Sbjct  446  CGCCAGGGTAGCCGGACTCAGCTGCGAGGAGATGGGCTTCCTCAG 490

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>gb|BC072688.1|  Rattus norvegicus hepsin, mRNA (cDNA clone MGC:91742 IMAGE:7098661), complete cds
Length=1580

GENE ID: 29135 Hpn | hepsin [Rattus norvegicus] (10 or fewer PubMed links)

Sort alignments for this subject sequence by:
E value Score Percent identity
Query start position Subject start position

Score = 935 bits (506), Expect = 0.0
Identities = 828/983 (84%), Gaps = 23/983 (2%)
Strand=Plus/Plus

```

Query  184  ACCCCAGGGTCCCACCTGGCCCAGGAGGTGAGCCAGGGAATCATTAACAAGAGGCAGTG 243
Sbjct  27  ACCCCAGGGTTCGCGCCCGAGCCCAACAGGTCAACCTGGGAATCATTAACAAGAGTCCCTG 86

Query  244  ACATGGCGCAGAAGGAGGGTGGCCGGACTGTGCCATGTGCTCCAGACCCAGGTGGCAG 303
Sbjct  87  ACAT-G-GC-GAAGGAGGGTGGCCGGACTGCACCATGTGTTCCAGACCCAGGTGGCAG 143

Query  304  CTCTCACTGCGGGGACCTGCTACTTC-TGACAGCCATCGGGGCGGCATCCTGGGCCATT 362
Sbjct  144  CTCTCACTGTGGGGACCTGCTG-TTCCTGACAGGCATTGGGGCTGCGTCTGGGCCATT 202

Query  363  GTGGCTGTCTCTCT-CAGGAGTGACCAGGAGCCGCTGTACCCAGTGACGGTCAG-CTCTG 420
Sbjct  203  GTGACCATCCTACTAC-GGAGTGACCAGGAGCCACTGTACCAAGTGACAGTCAGTCCCGG 261

Query  421  CGGACGCTCGGCTCATGGTCTTTGACAAGACGGAAGGGA-CGTGGCGGCTGCTGTGCTCC 479
Sbjct  262  -GGACTCTCGACTTTTGGTGTGGACAAGACAGA-GGGAACGTGAGGCTGCTGTGCTCC 319

Query  480  TCGCGCTCCAACGCCAGGGTAGCCGGACTCAGCTGCGAGGAGATGGGCTTCCTCAGGGCA 539
Sbjct  320  TCACGCTCCAACGCCAGGGTAGCAGGGCTCGGCTGTGAGGAGATGGGCTTTCTCAGGGCT 379

Query  540  CTGACCCACTCCGAGCTGGACGTGCGAACGCGGGCGCCAATGGCAGTCGGGCTTCTTC 599
Sbjct  380  CTGGCGCACTCAGAGCTGGATGTGCGAACGCGGGCGCCAACGGCACATCGGGCTTCTTC 439

Query  600  TGTGTGGACGAGGGGAGG-CTGCCCCACACCCAGAGGCTGCTGGAGGTGATCTCCGTGTG 658
Sbjct  440  TGCCTGGACGAGGGC-GGTCTGCCTCTGGCTCAGCGGTTGCTGGATGTCTCTGTATG 498

Query  659  TGATTGCCCCAGAGGCCGTTTCTTGCCCGCATCTGCCAAGACTGTGGCCGAGGAAGCT 718
Sbjct  499  CGACTGTCTTAGAGGCCGATTCTCTGACTGCCACCTGCCAAGACTGTGGCCGAGGAAGCT 558

Query  719  GCCCGTGGACCGCATCGTGGGAGGCCGGGACACCAGCTTGGGCGCGTGGCCGTGGCAAGT 778
Sbjct  559  GCCCGTGGATCGCATTTGTGGGGGGCAGGACAGCAGCCTGGGAAGATGGCCATGGCAGGT 618

Query  779  CAGCCTTCGCTATGATGG-AGCACACCTCTGTGGGGGATCCCTGCTCTCCGGGGACTGGG 837
Sbjct  619  CAGCCTTCGCTTATGATGGGACC-CACCTCTGTGGGGGATCCCTGCTGTCCGGGGACTGGG 677

Query  838  TGCTGACAGCCGCCACTGCTTCCCGAGCGGAACCGGGTCCTGTCCCGATGGCGAGTGT 897
Sbjct  678  TACTGACCGCTGCACACTGCTTTCCAGAGAGGAACCGGGTCCTGTCTCGGTGGCGAGTAT 737

Query  898  TTGCCGGTGGCCGTGGCCAGG-CCTCTCCCCACGGTC-TGCAGCTGGGGGTGCAGGCTGT 955
Sbjct  738  TTGTGTGTGCTGTAGCCC-GGACCTCACCTCATGC-CGTGCAGCTGGGGGTTCAGGCTGT 795

Query  956  GGTCTACCACGGGGGCTATCTTCCCTTTTCGGGACCCCAAC-AGCGAGGAGAACAGCAACG 1014
Sbjct  796  GATCTATCATGGGGGTACCTTCCCTTTTCGAGACCTA-CTATCGACGAAAACAGCAATG 854

Query  1015  ATATTGCCCTGGTCCACCTCTCCAG-TCCCTTGCCCTCACAGAATACATCCAGCCTGTG 1073
Sbjct  855  ACATTGCCCTGGTCCACCTCTCTAGCTCCC-TGCCTCTCACAGAATACATCCAGCCGGTG 913

Query  1074  TGCCTCCAGCTGCGCGCCAGGCCCTGGTGGATGGCAAGATCTGTACCGTGACGGGCTGG 1133
Sbjct  914  TGTCTCCTGCTGCGGGACAGGCCCTGGTGGACGGCAAGGTCTGTACAGTGACCGGCTGG 973

Query  1134  GGCAACACGCACTACTATGGCCA 1156
Sbjct  974  GGTAACACACAGTTCTATGGCCA 996

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Score = 265 bits (143), Expect = 6e-67
Identities = 405/525 (77%), Gaps = 44/525 (8%)
Strand=Plus/Plus

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Query  1291  GCCAGGGCGACAGCGGTGGTCCCTTTGTGTGTGAGGACAGCATCTCTCGG-ACGCCACGT 1349

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Sbjct  993      |GCCAGGGTGACAGCGGAGGCCCTTTGTATGTGAGGACAGAATCTCT-GGAACATCAAGA| 1051
Query  1350      |TGGCGGCTGTGTGGCATTGTGAGTTGGGGCACTGGCTGTGCCCTGGCCAGAACCCAGGC| 1409
Sbjct  1052      |TGGCGGCTGTGCGGCATTGTAAGCTGGGGTACGGGCTGTGCTTTGGCCCGGAAGCCGGGA| 1111
Query  1410      |GTCTACACCAAAGTCAGTGACTTCCGGGAGTGGATCTTCCAGGCCATAAAGACTCACTCC| 1469
Sbjct  1112      |GTGTACACCAAAGTCATTGACTTCCGGGAGTGGATCTTCCAGGCCATAAAGACTCACTCC| 1171
Query  1470      |GAAGCCAGCGGCATGGTGACCCAGCTCTGACCG-G--TG--GCTT-CTC-GC--TGCGC| 1519
Sbjct  1172      |GAAGCTACCGGCATGGTAACTCAGCCCTGACCCCGCCTCATCGCTGCTCCGCGCTGCTC| 1231
Query  1520      |-AGCTTCAGGGCCCGAG--G-T--GAT--C-CCGT-G--GTGGGA---TCCACGCTG| 1563
Sbjct  1232      |CAGCATCCAGAGTCAGAGTTGGTCTGGTGGCTCCAGCCGCACGTGGCAGGCTCCACACTG| 1291
Query  1564      |GGCCG-AGGATGGGACGTTTTTCTTCTTGGGCCCGGTCCACAGGTCCAAGGACACCTCC| 1622
Sbjct  1292      |GGCTCAC-ATGGAACGTTTTTCTGCTCGGATCCAGTCCATAGATCCAAGGATGC--TGG| 1348
Query  1623      |CTCCAGGGTCTCTCTTCCACAGTGGCGGGCCCACTCAGCCCC-GAGACCAACCAACCTC| 1681
Sbjct  1349      |GTCCAAGGACCTCTCTTCCACAGTGGCCGGCCCACTCAATCCAGGG-CCATTGG-CCTC| 1406
Query  1682      |ACCTCTCTGACCCCATGTAAATATTGTTCTG-CTGTCTGGGA-CTCCTGTCTAGGTGCC| 1739
Sbjct  1407      |ACCTCTCC-ACCCC-ATGTAAATATTACTCTGTCC-TCTGGGGGCTGCTTTTCGAGGCGCC| 1463
Query  1740      |CCTGATGATG-GGATGCTCTTTAAATAATAAAGATGGTTTTGATT 1783
Sbjct  1464      |CCT--TG-TGCGGATGCTCTTTAAATAATAAAGGTGGTTTTGATT 1505

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>gb|AY234104.1|  Mus musculus truncated hepsin splice variant mRNA, complete cds;
alternatively spliced
Length=1887

GENE ID: 15451 Hpn | hepsin [Mus musculus] (Over 10 PubMed links)

Sort alignments for this subject sequence by:
E value Score Percent identity
Query start position Subject start position

Score = 880 bits (476), Expect = 0.0
Identities = 944/1164 (81%), Gaps = 56/1164 (4%)
Strand=Plus/Plus

```

Query  658      |GTGATTGCCCCAGAGGCGGTTTCTTGGCCGCCATCTGCCAAGACTGTGGCCGCAGGAAGC| 717
Sbjct  720      |GTGACTGTCTTAGAGGCGGATTCTCTGACTGCCACCTGCCAAGACTGTGGCCGCAGGAAGC| 779
Query  718      |TGCCCGTGGACCGCATCGTGGGAGGCCGGACACCAG-CTTGGGCCGCTGGCCGTGGCAA| 776
Sbjct  780      |TGCCCGTGGACCGCATTGTGGGGGGCCAGGACAGCAGTCT-GGGAAGGTGGCCGTGGCAG| 838
Query  777      |GTCAGCCTTCGCTATGATGG-AGCACACCTCTGTGGGGGATCCCTGCTCTCCGGGACTG| 835
Sbjct  839      |GTCAGCCTGCGTTATGATGGGACC-CACCTCTGTGGGGGTCCCTGCTGTCTGGGGACTG| 897
Query  836      |GGTGCTGACAGCGCCCACTGCTTCCCGGAGCGGAACCGGGTCTGTCCCGATGGCGAGT| 895
Sbjct  898      |GGTGCTGACTGTGTCACATTGCTTTCCAGAGCGGAACCGGGTCTGTCTCGGTGGCGAGT| 957
Query  896      |GTTTGCCCGGTGCCGTGGCCCCAGG-CCTCTCCCCACGGTCTGCAGCTGGGGGTGCAGGCTG| 954
Sbjct  958      |ATTTGCTGGTGTGTAGCCC-GGACCTCACCCCATGCTGTGCAACTGGGGGTTCAGGCTG| 1016
Query  955      |TGGTCTACCAACGGGGGCTATCTTCCCTTTTCGGGACCCCAAC-AGCGAGGAGAACAGCAAC| 1013
Sbjct  1017      |TGATCTATCATGGGGGTACCTTCCCTTTTCGAGACCCTA-CTATTGACGAAAACAGCAAT| 1075
Query  1014      |GATATTGCCTTGGTCCACCTCTCCAG-TCCCTTGCCCTCACAGAATACATCCAGCCTGT| 1072
Sbjct  1076      |GACATTGCCTTGGTCCACCTCTCTAGCTCCC-TGCCTCTCACAGAATACATCCAGCCAGT| 1134
Query  1073      |GTGCCTCCCAGCTGCCGCCAGGCCCTGGTGGATGGCAAGATCTGTACCGTGACGGGCTG| 1132
Sbjct  1135      |GTGTCTCCCTGCTGCGGGACAGGCCCTGGTGGATGGCAAGGTCTGTACTGTGACCGGCTG| 1194
Query  1133      |GGGCAACACGCAGTACTATGGCCAAACAGGCCGGGGTACTCCAGGAGGCTCGAGTCCCCAT| 1192
Sbjct  1195      |GGGTAAACACACAGTTCTATGGCCAAACAGGCTATGGTGTCTCCAAGAGGCCCGGGTTCCCAT| 1254
Query  1193      |AATCAGCAATGATGTCTGCAATGGCGCTGACTTCTATGGAAACCAGATCAAGCCCAAGAT| 1252
Sbjct  1255      |CATAAGCAACGAAGTTTGCAACAGCCCCGACTTCTACGGGAATCAGATCAAGCCCAAGAT| 1314
Query  1253      |GTTCTGTGCTGGCTACCCCGAGGGTGGCATTGATGCCTGCCAGGGCGACAGCGGTGGTCC| 1312
Sbjct  1315      |GTTCTGTGCTGGCTATCTGAGGGTGGCATTGATGCGTGCCAGGGCGACAGTGGAGGCCCC| 1374
Query  1313      |CTTTGTGTGTGAGGACAGCATCTCTCGGACGCCACGTTGGCGGCTGTGTGGCATTGTGAG| 1372
Sbjct  1375      |CTTTGTGTGTGAAGACAGCATCTCTGGGACATCAAGGTGGCGGCTATGTGGCATTGTAAG| 1434

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Query 1373 TTGGGGCACTGGCTGTGCCCTGGCCCAGAAAGCCAGGCGTCTACACCAAAGTCAGTGACTT 1432
Sbjct 1435 CTGGGGTACCGGCTGTGCTTTGGCCCAGGAAGCCAGGAGTGTACACCAAAGTCAGTGACTT 1494
Query 1433 CCGGGAGTGGATCTTCCAGGCCATAAAGACTCACTCCGAAGCCAGCGGCATGGTGACCCA 1492
Sbjct 1495 CCGGGAGTGGATCTTCAAGGCCATAAAGACTCACTCCGAAGCCAGTGGCATGGTGACTCA 1554
Query 1493 GCTCTGA-CCGG--TGG-CT---T-CTC-G--CTGCGC-AGCCTCCAGGGCCCGAG--G- 1537
Sbjct 1555 GCCCTGATCCCGCCTCATCTCGCTGCTCCGTGCTGCACTAGCATCCAGAGTCAGAGTTGG 1614
Query 1538 T--GAT--C-CC-G-----GTGGTGGGATCCACGCTGGGCCG-AGGATGGGACGTTTTT 1584
Sbjct 1615 TCTGGTGGCTCCAGCCCCACGTGGTAGGCTCCCACTGGGCCCTCAC-ATGGAATGGTTTC 1673
Query 1585 CTTCTTGGGCCCCGTCCACAGGTCCAAGGACACCTCCCTCCAGGGTCCTCTCTTCCACA 1644
Sbjct 1674 CTGCTCAGATCCAGTCCACGGGTCCAAGGATGC--TGGATCCAAGGACTTCTCTTCCACA 1731
Query 1645 GTGGCGGGCCCACTCAGCCCC-GAGACCACCAACCTCACCTCCTGACCCCCATGTAAA 1703
Sbjct 1732 GTGGCCGGCCCACTCAATCCCAGGG-CCATTGG-CCTCACCTCCC-ACCCC-ATGTAAA 1787
Query 1704 TATTGTTCTG-CTGTCTGGGACTC-CTGTCTAGGT-GCCCCCTGATGATGG-GATGCTCTT 1759
Sbjct 1788 TATTACTCTGTCC-TCTGGGGGGCGCT--CTAGGGAGCCCCCT--TG-TGCAGATGCTCTT 1841
Query 1760 TAAATAATAAAGATGGTTTTGATT 1783
Sbjct 1842 TAAATAATAAAGGTGGTTTTGATT 1865


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Score = 403 bits (218), Expect = 1e-108
Identities = 394/477 (82%), Gaps = 19/477 (3%)
Strand=Plus/Plus

```

Query 184 ACCCCAGGGTCCCAACCTGGCCCAGGAGGTAGCCAGGGAAATCATTAACAAGAGGCAGTG 243
Sbjct 143 ACCCCAGGGTTCCGCCCCAGCCCAACAGGTCAACCTGGGAATCATTAACAAGAGTCCCTG 202
Query 244 ACATGGCGCAGAAAGGAGGGTGGCCGGACTG-TGCCATGCTGCTCCAGACCCAAGGTGGCA 302
Sbjct 203 ACAT-G-GC-GAAGGAGGGTGGCCGGACTGCAG-CATGCTGCTCCAGACCCAAGGTGGCA 258
Query 303 GCTCTCACTGCGGGGACCTGTACTTTC-TGACAGCCATCGGGCGGCATCCTGGGCCAT 361
Sbjct 259 GCTCTCATGTGTTGGGTACCCTGTG-TTCCTGACAGGCATTGGGGCCGCTCCTGGGCCAT 317
Query 362 TGTGGCTGTTCTCTCT-CAGGAGTGACAGGAGCCGCTGTACCCAGTGCAAGTCAAGTCT- 419
Sbjct 318 TGTGACCATCTCTACTGCAG-AGTGACAGGAGCCACTGTACCAAGTGCAGCTCAG-TCCA 375
Query 420 GCGGACGCTCGGCT--CATGGTCTTTGACAAGACGGAAGGG-ACGTGGCGGCTGCTGTGC 476
Sbjct 376 GGGGACTCAGACTTGCA-G-TGTTGGACAAGACGGA-GGGTACGTGGAGGCTACTGTGC 432
Query 477 TCCTCGCGCTCCAACGCCAGGGTAGCCGGAATCAGCTGCGAGGAGATGGGCTTCTCAGG 536
Sbjct 433 TCCTCAGCTCCAATGCCAGGGTGGCAGGGCTCGGCTGTGAGGAGATGGGCTTCTCAGG 492
Query 537 GCACTGACCCACTCCGAGCTGGACGTGCGAACGGCGGGCGCCAATGGCAGTGGGGCTTC 596
Sbjct 493 GCTCTGGCGCACTCGGAGCTGGATGTGCGCACTGCGGGCGCCAACGGCAGTGGGGCTTC 552
Query 597 TTCTGTGTGGACGAGGGGAGG-CTGCCCCACCCAGAGGCTGCTGGAGGTATCTC 652
Sbjct 553 TTTTGCCTGGACGAGGGG-GGACTGCCTCTGGCTCAGAGGTTGCTGGATGTATCTC 608

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>ref|XM_001254640.1|  PREDICTED: Bos taurus similar to hepsin (LOC787164), partial mRNA
Length=779

GENE ID: 787164 LOC787164 | similar to hepsin [Bos taurus]

Score = 815 bits (441), Expect = 0.0
Identities = 662/761 (86%), Gaps = 46/761 (6%)
Strand=Plus/Plus

```

Query 1052 CACAGAATACATCCAGCCTGTGTGCCTCCAGCTGCCGGCCAGGCCCTGGTGGATGGCAA 1111
Sbjct 34 CACAGAGTACATCCAGCCCGTGTGTCTCCCGGCTGCCGGGCAGGCCCTGGTGGATGGCAA 93
Query 1112 GATCTGTACCGTGACGGGCTGGGGCAACACGCACTACTATGGCCAACAGGCCGGGGTACT 1171
Sbjct 94 GATCTGCACGGTGAAGGCTGGGGCAACACGCACTACTACGGCCAACAGGCTGGGGTGCT 153
Query 1172 CCAGGAGGCTCGAGTCCCCATAATCAGCAATGATGTCTGCAATGGCGCTGACTTCTATGG 1231
Sbjct 154 CCAGGAGGCGCGAGTCCCCATAATCAGCAATGATGTCTGCAACGGCCCCGACTTCTACGG 213
Query 1232 AAACAGATCAAGCCCCAAGATGTTCTGTGCTGGCTACCCCGAGGGTGGCATTGATGCCTG 1291
Sbjct 214 GAACAGATCAAGCCCCAAGATGTTCTGTGCTGGCTACCCCGAGGGTGGCATTGATGCCTG 273

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Query 1292 CCAGGGCGACAGCGGTGGTCCCTTTGTGTGTGAGGACAGCATCTCTCGGACGCCACGTTG 1351
Sbjct 274 CCAGGGCGACAGTGGTGGCCCTTCGTGTGTGAGGATAGCATCTCTCGGACGCCACGTTG 333
Query 1352 GCGGCTGTGTGGCATTGTGAGTTGGGGCACTGGCTGTGCCCTGGCCAGAAAGCCAGGCGT 1411
Sbjct 334 GCGGCTGTGTGGCATTGTGAGCTGGGGCAACGGCTGTGCCCTGGCCAGAAAGCCAGGCGT 393
Query 1412 CTACACCAAAGTCAGTGACTTCCGGGAGTGGATCTTCCAGGCCATAAAGACTCACTCCGA 1471
Sbjct 394 CTACACCAAAGTCAGTGACTTCCGGGAGTGGATCTTCCAGGCCATAAAGACTCACTCCGA 453
Query 1472 AGCCAGCGGCATGGTGACCCAGCTCTGACCGGTGGCTTCTC---GCTGCGCA-GCCTCCA 1527
Sbjct 454 AGCCAGCGGCATGGTAACCCAGCTTTGACCTGTGGCTTCTCCTCGCTGTGCACGCCTCCA 513
Query 1528 GGGCCCGAGGTGATC-----CC---G-----GTGGTGGGATCCACGCTGGGCCGAGG 1571
Sbjct 514 GGGCCCGAGCTGATCTAAGGGGCCCCAGCCCCACGTGATGGGGTTACCCCTGGGCC-AGG 572
Query 1572 -ATGGGACGTTTTTCTTCTTGGGCCCGGTCCACAGGTCCAAGGACACCCT-CCCTCCAGG 1629
Sbjct 573 GATGGAACATTTTTCTTCTTGGGCCCAGCCACAGGTCCAAGGATACTCTTCCCTCCAAG 632
Query 1630 GTCCTCTCTTCCACAGTGGCGGGCCCACTCAGCCCCGAGACCACCCAACTCACCCTCCT 1689
Sbjct 633 GTCTCTC-C---ACAGTGGCGGGCCCACTCAGCCCTGGGACCACCC---TC-C--TGC- 679
Query 1690 GACCCCATGTAAATATGTCTGTCTGCGGA-CTCCTG-----TCTAGGTGCCCT 1742
Sbjct 680 --CCCCCATGTAAATATGTCTGTCCATCTGGGATCCCCCCCCCATCTTG-TGCTCCT 736
Query 1743 GATGATGGGATGCTCTTTAAATAATAAAGATGGTTTTGATT 1783
Sbjct 737 GAAGACAGGATGCTCTTTAAATAATAAAGATGGTTTTGATT 777

```

>gb|BC119448.1| Mus musculus cDNA clone IMAGE:40044314
Length=772

Score = 717 bits (388), Expect = 0.0
Identities = 633/752 (84%), Gaps = 14/752 (1%)
Strand=Plus/Minus

```

Query 448 AGACGGAAGGG-ACGTGGCGGTGCTGTGCTCCTCGCGTCCAACGCCAGGGTAGCCGGA 506
Sbjct 761 AGA-GGATGGGAACGTGGAGGCTACTGTGCTCCTCACGCTCCAATGCCAGGGTGGCAGGG 703
Query 507 CTCAGTGTGCGAGGAGATGGGCTTCTCAGGGCACTGACCCACTCCGAGCTGGACGTGCGA 566
Sbjct 702 CTCGGCTGTGAGGAGATGGGCTTCTCAGGGCTCTGGCACACTCGGAGCTGGATGTGCGC 643
Query 567 ACGGCGGGCGCCAATGGCACGTCGGGCTTCTTCTGTGTGGACGAGGGGAGG-CTGCCCA 625
Sbjct 642 ACTGCGGGCGCCAACGCGCACATCGGGCTTCTTTGCGTGGACGA-GGGCGGACTGCCTCT 584
Query 626 CACCAGAGGGTGTCTGGAGGTATCTCCGTGTGTGATTGCCCCAGAGGCCGTTTCTTGGC 685
Sbjct 583 GGCTCAGAGGTTGCTGGATGTATCTCTGTATGTGACTGTCTAGAGGCCGATTCTCTGAC 524
Query 686 CGCCATCTGCCAAGACTGTGGCCGCAAGAGCTGCCCGTGGACCGCATCGTGGGAGGCCG 745
Sbjct 523 TGCCACCTGCCAAGACTGTGGCCGCAAGAGCTGCCCGTGGACCGCATGTGGGGGGCCA 464
Query 746 GGACACCAG-CTTGGGCCGGTGGCCGTGGCAAGTCAGCCTTCGCTATGATGG-AGCACAC 803
Sbjct 463 GGACAGCAGTCT-GGGAAGGTGGCCGTGGCAGGTCAGCCTGCGTTATGATGGGACC-CAC 406
Query 804 CTCTGTGGGGGATCCCTGCTCTCCGGGGACTGGGTGCTGACAGCCGCCCACTGCTTCCCG 863
Sbjct 405 CTCTGTGGGGGTCCCTGCTGTCTGGGGACTGGGTGCTGACTGCTGCACATTGCTTTCCA 346
Query 864 GAGCGGAACCGGGTCTGTCTCCGATGGCGAGTGTGTGCCGGTGCCGTGGCCAGG-CCTC 922
Sbjct 345 GAGCGGAACCGGGTCTGTCTCGGTGGCGAGTATTTGCTGGTGTGTAGCCC-GGACCTC 287
Query 923 TCCCCACGGTCTGCAGCTGGGGGTGCAGGCTGTGGTCTACCAGGGGGCTATCTTCCCTT 982
Sbjct 286 ACCCCATGCTGTGCAACTGGGGGTTAGGCTGTGATCTATCATGGGGGCTACCTTCCCTT 227
Query 983 TCGGGACCCCAAC-AGCGAGGAGAACAGCAACGATATTGCCCTGGTCCACCTCTCCAG-T 1040
Sbjct 226 TCGAGACCTTA-CTATCGACGAAAAAGCAATGACATTGCCTTGGTCCACCTCTCTAGCT 168
Query 1041 CCCCTGCCCTCTACAGAATACATCCAGCCTGTGTGCCTCCAGCTGCCGGCCAGGCCCTG 1100
Sbjct 167 CCC-TGCCTCTACAGAATACATCCAGCCAGTGTGTCTCCCTGCTGCGGGACAGGCCCTG 109
Query 1101 GTGGATGGCAAGATCTGTACCGTGACGGGCTGGGGCAACACGAGTACTATGGCCAACAG 1160
Sbjct 108 GTGGATGGCAAGGTCTGTACTGTGACCGGCTGGGGTAACACACAGTTCTATGGCCAACAG 49
Query 1161 GCCGGGGTACTCCAGGAGGCTCGAGTCCCCAT 1192
Sbjct 48 GCTATGGTGTCTCAAGAGGCCCGGGTTCCCAT 17

```

>gb|BC119449.1| Mus musculus cDNA clone IMAGE:40044315

Length=772

Score = 712 bits (385), Expect = 0.0
Identities = 632/752 (84%), Gaps = 14/752 (1%)
Strand=Plus/Minus

```
Query 448 AGACGGAAGGG-ACGTGGCGGCTGCTGTGCTCCTCGCGCTCCAACGCCAGGGTAGCCGGA 506
Sbjct 761 AGA-GGATGGGAACGTGGAGGCTACTGTGCTCCTCACGCTCCAATGCCAGGGTGGCAGGG 703

Query 507 CTCAGCTGCGAGGAGATGGGCTTCTCAGGGCACTGACCCACTCCGAGCTGGACGTGCGA 566
Sbjct 702 CTCGGCTGTGAGGAGATGGGCTTCTCAGGGCTCTGGCACACTCGAGCTGGATGTGCGC 643

Query 567 ACGGCGGGCGCCAATGGCACGTCGGGCTTCTTCTGTGTGGACGAGGGGAGG-CTGCCCCA 625
Sbjct 642 ACTGCGGGCGCCAACGGCACATCGGGCTTCTTTTACGTGGACGA-GGGCGGACTGCCTCT 584

Query 626 CACCAGAGGGTGTCTGGAGGTCACTCCCGTGTGTGATTGCCCCAGAGGCCGTTTCTTGGC 685
Sbjct 583 GGCTCAGAGGTTGTCTGGATGTATCTCTGTATGTGACTGTCCTAGAGGCCGATTCTCTGAC 524

Query 686 CGCCATCTGCCAAGACTGTGGCCGAGGAAGCTGCCCCGAGACCGCATCGTGGGAGGCCG 745
Sbjct 523 TGCCACCTGCCAAGACTGTGGCCGAGGAAGCTGCCGGTGGACCGCATTGTGGGGGGCCA 464

Query 746 GGACACCAG-CTTGGGCGGGTGGCCGTGGCAAGTCAGCCTTCGCTATGATGG-AGCACAC 803
Sbjct 463 GGACAGCAGTCT-GGGAAGGTGGCCGTGGCAGGTCAGCCTGCGTTATGATGGGACC-CAC 406

Query 804 CTCTGTGGGGGATCCCTGCTCTCCGGGGACTGGGTGCTGACAGCCGCCCACTGCTTCCCG 863
Sbjct 405 CTCTGTGGGGGTCCTCTGCTGTCTGGGGACTGGGTGCTGACTGCTGCACATTGCTTTCCA 346

Query 864 GAGCGGAACCGGGTCTGTCTCCGATGGCGAGTGTGTGCCGGTGCCGTGGCCCAAGG-CCTC 922
Sbjct 345 GAGCGGAACCGGGTCTGTCTCGGTGGCGAGTATTTGCTGGTGTGTAGCCC-GGACCTC 287


Query 923 TCCCCACGGTCTGCAGCTGGGGGTGCAGGCTGTGGTCTACCACGGGGGCTATCTTCCCTT 982
Sbjct 286 ACCCCATGCTGTGCAACTGGGGGTTAGGCTGTGATCTATCATGGGGGCTACCTTCCCTT 227

Query 983 TCGGGACCCCAAC-AGCGAGGAGAAAGCAACGATATTGCCCTGGTCCACCTCTCCAG-T 1040
Sbjct 226 TCGAGACCTTA-CTATCGACGAAAAAGCAATGACATTGCCTTGGTCCACCTCTCTAGCT 168

Query 1041 CCCCTGCCCTCTACAGAATACATCCAGCCTGTGTGCTTCCAGCTGCCGGCCAGGCCCTG 1100
Sbjct 167 CCC-TGCCTCTACAGAATACATCCAGCCAGTGTGTCTCCCTGCTGCGGGACAGGCCCTG 109

Query 1101 GTGGATGGCAAGATCTGTACCGTGAAGGGTGGGGCAACACGAGTACTATGGCCAACAG 1160
Sbjct 108 GTGGATGGCAAGGTCTGTACTGTGACCGGTGGGGTAACACAGATTCTATGGCCAACAG 49

Query 1161 GCCGGGGTACTCCAGGAGGCTCGAGTCCCAT 1192
Sbjct 48 GCTATGGTGCTCCAAGAGGCCCGGTTCCCAT 17
```

>gb|AC192150.4|  Pan troglodytes BAC clone CH251-522E19 from chromosome 19, complete
sequence
Length=213011

Sort alignments for this subject sequence by:
E value Score Percent identity
Query start position Subject start position

Score = 590 bits (319), Expect = 9e-165
Identities = 323/325 (99%), Gaps = 0/325 (0%)
Strand=Plus/Plus

```
Query 1459 AGACTCACTCCGAAGCCAGCGGCATGGTGACCCAGCTCTGACCGGTGGCTTCTCGCTGCG 1518
Sbjct 179133 AGACTCACTCCGAAGCCAGCGGCATGGTGACCCAGCTCTGACCGGTGGCTTCTCGCTGCG 179192

Query 1519 CAGCCTCCAGGGCCCGAGGTGATCCCGTGGTGGGATCCACGCTGGGCCGAGGATGGGAC 1578
Sbjct 179193 CAGCCTCCAGGGCCCGAGGTGATCCCGTGGTGGGATCCACGCTGGGCCGAGGATGGGAC 179252

Query 1579 GTTTTCTTCTTGGGCCCCGTCCACAGGTCCAAGGACACCCTCCCTCCAGGGTCTCTCT 1638
Sbjct 179253 GTTTTCTTCTTGGGCCCCGTCCACAGGTCCAAGGACACCCTCCCTCCAGGGTCTCTCT 179312

Query 1639 TCCACAGTGGCGGGCCCACTCAGCCCCGAGACACCCAACTCACCTCCTGACCCCCAT 1698
Sbjct 179313 TCCACAGTGGCGGGCCCACTCAGCCCCGAGACACCCAACTCACCTCCTGACCCCCAT 179372

Query 1699 GTAAATATTGTTCTGCTGTCTGGGACTCCTGTCTAGGTGCCCTGATGATGGGATGCTCT 1758
Sbjct 179373 GTAAATATTGTTCTGCTGTCTGGGACTCCTGTCTAGGTGCCCTGATGACGGGATGCTCT 179432

Query 1759 TTAAATAATAAAGATGGTTTGGATT 1783
Sbjct 179433 TTAAATAATAAAGATGGTTTGGATT 179457
```

Score = 348 bits (188), Expect = 6e-92

Identities = 198/202 (98%), Gaps = 3/202 (1%)
Strand=Plus/Plus

```

Query   858      TTCCC-GG-A-GCGGAACCGGGTCTGTCCCGATGGCGAGTGTGTTGCCGGTGCCGTGGCC   914
Sbjct   173569     TTCCCTGGTAGGCGGAACCGGGTCTGTCCCGATGGCGAGTGTGTTGCCGGTGCCGTGGCC   173628

Query   915      CAGGCCCTCTCCCCACGGTCTGCAGCTGGGGGTGCAGGCTGTGGTCTACCAACGGGGGCTAT   974
Sbjct   173629     CAGGCCCTCTCCCCACGGCTGCAGCTGGGGGTGCAGGCTGTGGTCTACCAACGGGGGCTAT   173688

Query   975      CTTCCCTTTTCGGGACCCCAACAGCGAGGAGAAACAGCAACGATATTGCCCTGGTCCACCTC   1034
Sbjct   173689     CTTCCCTTTTCGGGACCCCAACAGCGAGGAGAAACAGCAACGATATTGCCCTGGTCCACCTC   173748

Query   1035      TCCAGTCCCCTGCCCTTCACAG      1056
Sbjct   173749     TCCAGTCCCCTGCCCTTCACAG      173770

```

Score = 315 bits (170), Expect = 6e-82
Identities = 172/173 (99%), Gaps = 0/173 (0%)
Strand=Plus/Plus

```

Query   1288      CCTGCCAGGGCGACAGCGGTGGTCCCTTTGTGTGTGAGGACAGCATCTCTCGGACGCCAC   1347
Sbjct   178746     CCTCCAGGGCGACAGCGGTGGTCCCTTTGTGTGTGAGGACAGCATCTCTCGGACGCCAC   178805

Query   1348      GTTGGCGGCTGTGTGGCATTGTGAGTTGGGGCACTGGCTGTGCCCTGGCCAGAACCCAG   1407
Sbjct   178806     GTTGGCGGCTGTGTGGCATTGTGAGTTGGGGCACTGGCTGTGCCCTGGCCAGAACCCAG   178865

Query   1408      GCGTCTACACCAAAGTCAGTGACTTCCGGGAGTGGATCTTCCAGGCCATAAAG      1460
Sbjct   178866     GCGTCTACACCAAAGTCAGTGACTTCCGGGAGTGGATCTTCCAGGCCATAAAG      178918

```

Score = 313 bits (169), Expect = 2e-81
Identities = 172/173 (99%), Gaps = 1/173 (0%)
Strand=Plus/Plus

```

Query   695      CCA-AGACTGTGGCCGACAGGAAGCTGCCCGTGGACCGCATCGTGGGAGGCCGGGACACCA   753
Sbjct   173295     CCACAGACTGTGGCCGACAGGAAGCTGCCCGTGGACCGCATCGTGGGAGGCCGGGACACCA   173354

Query   754      GCTTGGGCCGGTGGCCGTGGCAAGTCAGCCTTCGCTATGATGGAGCACACCTCTGTGGGG   813
Sbjct   173355     GCTTGGGCCGGTGGCCGTGGCAAGTCAGCCTTCGCTATGATGGAGCACACCTCTGTGGGG   173414

Query   814      GATCCCTGCTCTCCGGGGACTGGGTGCTGACAGCCGCCCACTGCTTCCCGGAG      866
Sbjct   173415     GATCCCTGCTCTCCGGGGACTGGGTGCTGACAGCCGCCCACTGCTTCCCGGAG      173467

```

Score = 289 bits (156), Expect = 4e-74
Identities = 156/156 (100%), Gaps = 0/156 (0%)
Strand=Plus/Plus

```

Query   38      CAGGTGAGGCAGCCTGGCCTAGCAGGCCCAACGCCACCGCCTCTGCCTCCAGGCCGCCCG   97
Sbjct   154680     CAGGTGAGGCAGCCTGGCCTAGCAGGCCCAACGCCACCGCCTCTGCCTCCAGGCCGCCCG   154739

Query   98      CTGCTGCGGGGCCACCATGCTCCTGCCAGGCCTGGAGACTGACCCGACCCCGCACTAC   157
Sbjct   154740     CTGCTGCGGGGCCACCATGCTCCTGCCAGGCCTGGAGACTGACCCGACCCCGCACTAC   154799

Query   158      CTCGAGGCTCCGCCCCACCTGCTGGACCCCAAGGGT      193
Sbjct   154800     CTCGAGGCTCCGCCCCACCTGCTGGACCCCAAGGGT      154835

```

Score = 268 bits (145), Expect = 5e-68
Identities = 145/145 (100%), Gaps = 0/145 (0%)
Strand=Plus/Plus

```

Query   1152      GGCCAAACAGGCCGGGGTACTCCAGGAGGCTCGAGTCCCCATAATCAGCAATGATGTCTGC   1211
Sbjct   178425     GGCCAAACAGGCCGGGGTACTCCAGGAGGCTCGAGTCCCCATAATCAGCAATGATGTCTGC   178484

Query   1212      AATGGCGCTGACTTCTATGGAACACAGATCAAGCCCAAGATGTTCTGTGCTGGCTACCCC   1271
Sbjct   178485     AATGGCGCTGACTTCTATGGAACACAGATCAAGCCCAAGATGTTCTGTGCTGGCTACCCC   178544

Query   1272      GAGGGTGGCATTGATGCCTGCCAGG      1296
Sbjct   178545     GAGGGTGGCATTGATGCCTGCCAGG      178569

```

Score = 248 bits (134), Expect = 6e-62
Identities = 134/134 (100%), Gaps = 0/134 (0%)
Strand=Plus/Plus

```

Query   403      CAGTGCAGGTCAGCTCTGCGGACGCTCGGCTCATGGTCTTTGACAAGACGGAAGGGACGT   462
Sbjct   172624     CAGTGCAGGTCAGCTCTGCGGACGCTCGGCTCATGGTCTTTGACAAGACGGAAGGGACGT   172683

Query   463      GGCGGCTGCTGTGCTCCTCGCGCTCCAACGCCAGGGTAGCCGGAAGCTCAGCTGCGAGGAGA   522

```

```

Sbjct  172684  GCGGGCTGCTGTGCTCCTCGCGTCCAACGCCAGGGTAGCCGGACTCAGCTGCGAGGAGA  172743
Query   523      TGGGCTTCCTCAGG  536
Sbjct  172744  TGGGCTTCCTCAGG  172757

```

Score = 228 bits (123), Expect = 8e-56
 Identities = 128/130 (98%), Gaps = 1/130 (0%)
 Strand=Plus/Plus

```

Query   533      CAGGGCACTGACCCACTCCGAGCTGGACGTGCGAACGGCGGGCGCCAATGGCACGTCGGG  592
Sbjct  172825  CAGGGCACTGACCCACTCCGAGCTGGACGTGCGAACGGCGGGCGCCAATGGCACGTCGGG  172884
Query   593      CTCTTCTGTGTGGACGAGGGGAGGCTGCCCCACACCCAGAGGCTGCTGGAGGTCATCTC  652
Sbjct  172885  CTCTTCTGCGTGGACGAGGGGAGGCTGCCCCACACCCAGAGGCTGCTGGAGGTCATCTC  172944
Query   653      CGTGTG-TGA  661
Sbjct  172945  CGTGTGGTGA  172954

```

Score = 191 bits (103), Expect = 1e-44
 Identities = 103/103 (100%), Gaps = 0/103 (0%)
 Strand=Plus/Plus

```

Query   261      GGTGGCCGGACTGTGCCATGCTGTCCAGACCCAAGGTGGCAGCTCTCACTGCGGGGACC  320
Sbjct  162138  GGTGGCCGGACTGTGCCATGCTGTCCAGACCCAAGGTGGCAGCTCTCACTGCGGGGACC  162197
Query   321      CTGCTACTTCTGACAGCCATCGGGGCGGCATCCTGGGCCATTG  363
Sbjct  162198  CTGCTACTTCTGACAGCCATCGGGGCGGCATCCTGGGCCATTG  162240

```

Score = 189 bits (102), Expect = 4e-44
 Identities = 102/102 (100%), Gaps = 0/102 (0%)
 Strand=Plus/Plus

```

Query   1052     CACAGAATACATCCAGCCTGTGTGCCTCCAGCTGCCGGCCAGGCCCTGGTGGATGGCAA  1111
Sbjct  178132  CACAGAATACATCCAGCCTGTGTGCCTCCAGCTGCCGGCCAGGCCCTGGTGGATGGCAA  178191
Query   1112     GATCTGTACCGTGACGGGCTGGGGCAACACGCAGTACTATGG  1153
Sbjct  178192  GATCTGTACCGTGACGGGCTGGGGCAACACGCAGTACTATGG  178233

```

Score = 137 bits (74), Expect = 1e-28
 Identities = 74/74 (100%), Gaps = 0/74 (0%)
 Strand=Plus/Plus

```

Query   191      GGTCCCACCCTGGCCCAGGAGGTGAGCCAGGGAATCATTAACAAGAGGCAGTGACATGGC  250
Sbjct  155413  GGTCCCACCCTGGCCCAGGAGGTGAGCCAGGGAATCATTAACAAGAGGCAGTGACATGGC  155472
Query   251      GCAGAAGGAGGGTG  264
Sbjct  155473  GCAGAAGGAGGGTG  155486

```

Score = 80.5 bits (43), Expect = 2e-11
 Identities = 43/43 (100%), Gaps = 0/43 (0%)
 Strand=Plus/Plus

```

Query   363      GTGGCTGTTCTCCTCAGGAGTGACCAGGAGCCGCTGTACCCAG  405
Sbjct  162323  GTGGCTGTTCTCCTCAGGAGTGACCAGGAGCCGCTGTACCCAG  162365

```

Score = 78.7 bits (42), Expect = 9e-11
 Identities = 42/42 (100%), Gaps = 0/42 (0%)
 Strand=Plus/Plus

```

Query   658      GTGATTGCCCCAGAGGCCGTTTCTTGGCCGCCATCTGCCAAG  699
Sbjct  173082  GTGATTGCCCCAGAGGCCGTTTCTTGGCCGCCATCTGCCAAG  173123

```

>dbj|AK091988.1| Homo sapiens cDNA FLJ34669 fis, clone LIVER2001051
 Length=2547

Sort alignments for this subject sequence by:
 E value Score Percent identity
 Query start position Subject start position

Score = 590 bits (319), Expect = 9e-165
 Identities = 323/325 (99%), Gaps = 0/325 (0%)
 Strand=Plus/Plus

```

Query   1459     AGACTCACTCCGAAGCCAGCGGCATGGTGACCCAGCTCTGACCGGTGGCTTCTCGCTGCG  1518
Sbjct  2223     AGACTCACTCCGAAGCCAGCGGCATGGTGACCCAGCTCTGACCGGTGGCTTCTCGCTGCG  2282
Query   1519     CAGCCTCCAGGGCCGAGGTGATCCCGGTGGTGGGATCCACGCTGGGCCGAGGATGGGAC  1578

```



```

Sbjct  2283  |||CAGCCTCCAGGGCCCGAGGTGATCCCGGTGGTGGGATCCACGCTGGGCCTAGGATGGGAC||| 2342
Query   1579  GTTTTCTTCTTGGGCCCGGTCCACAGGTCCAAGGACACCCCTCCCTCCAGGGTCCTCTCT 1638
Sbjct  2343  GTTTTCTTCTTGGGCCCGGTCCACAGGTCCAAGGACACCCCTCCCTCCAGGGTCCTCTCT 2402
Query   1639  TCCACAGTGGCGGGCCCACTCAGCCCCGAGACCACCAACCTCACCTCCTGACCCCCAT 1698
Sbjct  2403  TCCACAGTGGCGGGCCCACTCAGCCCCGAGACCACCAACCTCACCTCCTGACCCCCAT 2462
Query   1699  GTAAATATTGTTCTGCTGTCTGGGACTCCTGTCTAGGTGCCCTGATGATGGGATGCTCT 1758
Sbjct  2463  GTAAATATTGTTCTGCTGTCTGGGACTCCTGTCTAGGTGCCCTGATGACGGGATGCTCT 2522
Query   1759  TTAAATAATAAAGATGGTTTTGATT 1783
Sbjct  2523  TTAAATAATAAAGATGGTTTTGATT 2547

```

Score = 315 bits (170), Expect = 6e-82
 Identities = 172/173 (99%), Gaps = 0/173 (0%)
 Strand=Plus/Plus

```

Query   1288  CCTGCCAGGGCGACAGCGGTGGTCCCTTTGTGTGTGAGGACAGCATCTCTCGGACGCCAC 1347
Sbjct  1836  CCTCCCAGGGCGACAGCGGTGGTCCCTTTGTGTGTGAGGACAGCATCTCTCGGACGCCAC 1895
Query   1348  GTTGGCGGTGTGTGGCATTGTGAGTTGGGGCACTGGCTGTGCCCTGGCCCAGAAGCCAG 1407
Sbjct  1896  GTTGGCGGTGTGTGGCATTGTGAGTTGGGGCACTGGCTGTGCCCTGGCCCAGAAGCCAG 1955
Query   1408  GCGTCTACACCAAAGTCAGTGACTTCCGGGAGTGGATCTTCAGGCCATAAAG 1460
Sbjct  1956  GCGTCTACACCAAAGTCAGTGACTTCCGGGAGTGGATCTTCAGGCCATAAAG 2008

```

Score = 268 bits (145), Expect = 5e-68
 Identities = 145/145 (100%), Gaps = 0/145 (0%)
 Strand=Plus/Plus

```

Query   1152  GGCCAAACAGGCCGGGTACTCCAGGAGGCTCGAGTCCCCATAATCAGCAATGATGTCTGC 1211
Sbjct  1514  GGCCAAACAGGCCGGGTACTCCAGGAGGCTCGAGTCCCCATAATCAGCAATGATGTCTGC 1573
Query   1212  AATGGCGCTGACTTCTATGGAACACAGATCAAGCCCAAGATGTTCTGTGCTGGCTACCCC 1271
Sbjct  1574  AATGGCGCTGACTTCTATGGAACACAGATCAAGCCCAAGATGTTCTGTGCTGGCTACCCC 1633
Query   1272  GAGGGTGGCATTGATGCCTGCCAGG 1296
Sbjct  1634  GAGGGTGGCATTGATGCCTGCCAGG 1658

```

Score = 193 bits (104), Expect = 3e-45
 Identities = 104/104 (100%), Gaps = 0/104 (0%)
 Strand=Plus/Plus

```

Query   1050  CTCACAGAATACATCCAGCCTGTGTGCCTCCAGCTGCCGGCCAGGCCCTGGTGGATGGC 1109
Sbjct  1219  CTCACAGAATACATCCAGCCTGTGTGCCTCCAGCTGCCGGCCAGGCCCTGGTGGATGGC 1278
Query   1110  AAGATCTGTACCGTGACGGGCTGGGGCAACACGCAGTACTATGG 1153
Sbjct  1279  AAGATCTGTACCGTGACGGGCTGGGGCAACACGCAGTACTATGG 1322

```

>gb|AC020907.6|  Homo sapiens chromosome 19 clone CTD-252I21, complete sequence
 Length=169891

Sort alignments for this subject sequence by:
 E value Score Percent identity
 Query start position Subject start position

Score = 590 bits (319), Expect = 9e-165
 Identities = 323/325 (99%), Gaps = 0/325 (0%)
 Strand=Plus/Plus

```

Query   1459  AGACTCACTCCGAAGCCAGCGGCATGGTGACCCAGCTCTGACCGGTGGCTTCTCGCTGCG 1518
Sbjct  79750  AGACTCACTCCGAAGCCAGCGGCATGGTGACCCAGCTCTGACCGGTGGCTTCTCGCTGCG 79809
Query   1519  CAGCCTCCAGGGCCCGAGGTGATCCCGGTGGTGGGATCCACGCTGGGCCGAGGATGGGAC 1578
Sbjct  79810  CAGCCTCCAGGGCCCGAGGTGATCCCGGTGGTGGGATCCACGCTGGGCCGAGGATGGGAC 79869
Query   1579  GTTTTCTTCTTGGGCCCGGTCCACAGGTCCAAGGACACCCCTCCCTCCAGGGTCCTCTCT 1638
Sbjct  79870  GTTTTCTTCTTGGGCCCGGTCCACAGGTCCAAGGACACCCCTCCCTCCAGGGTCCTCTCT 79929
Query   1639  TCCACAGTGGCGGGCCCACTCAGCCCCGAGACCACCAACCTCACCTCCTGACCCCCAT 1698
Sbjct  79930  TCCACAGTGGCGGGCCCACTCAGCCCCGAGACCACCAACCTCACCTCCTGACCCCCAT 79989
Query   1699  GTAAATATTGTTCTGCTGTCTGGGACTCCTGTCTAGGTGCCCTGATGATGGGATGCTCT 1758
Sbjct  79990  GTAAATATTGTTCTGCTGTCTGGGACTCCTGTCTAGGTGCCCTGATGACGGGATGCTCT 80049

```

Query 1759 TTAAATAATAAAGATGGTTTTGATT 1783
Sbjct 80050 TTAAATAATAAAGATGGTTTTGATT 80074

Score = 353 bits (191), Expect = 1e-93
Identities = 199/202 (98%), Gaps = 3/202 (1%)
Strand=Plus/Plus

Query 858 TTCCC-GG-A-GCGGAACCGGGTCTGTCCCGATGGCGAGTGTGTCGGGTGCCGTGGCC 914
Sbjct 74119 TTCCCTGGTAGGCGGAACCGGGTCTGTCCCGATGGCGAGTGTGTCGGGTGCCGTGGCC 74178
Query 915 CAGGCCTCTCCCCACGGTCTGCAGCTGGGGGTGCAGGCTGTGGTCTACCACGGGGGCTAT 974
Sbjct 74179 CAGGCCTCTCCCCACGGTCTGCAGCTGGGGGTGCAGGCTGTGGTCTACCACGGGGGCTAT 74238
Query 975 CTTCCCTTTTCGGGACCCCAACAGCGAGGAGAACAGCAACGATATTGCCCTGGTCCACCTC 1034
Sbjct 74239 CTTCCCTTTTCGGGACCCCAACAGCGAGGAGAACAGCAACGATATTGCCCTGGTCCACCTC 74298
Query 1035 TCCAGTCCCCTGCCCCTCACAG 1056
Sbjct 74299 TCCAGTCCCCTGCCCCTCACAG 74320

Score = 315 bits (170), Expect = 6e-82
Identities = 172/173 (99%), Gaps = 0/173 (0%)
Strand=Plus/Plus

Query 1288 CCTGCCAGGGCGACAGCGGTGGTCCCTTTGTGTGTGAGGACAGCATCTCTCGGACGCCAC 1347
Sbjct 79363 CCTCCAGGGCGACAGCGGTGGTCCCTTTGTGTGTGAGGACAGCATCTCTCGGACGCCAC 79422
Query 1348 GTTGGCGGCTGTGTGGCATTGTGAGTTGGGGCACTGGCTGTGCCCTGGCCCAGAAGCCAG 1407
Sbjct 79423 GTTGGCGGCTGTGTGGCATTGTGAGTTGGGGCACTGGCTGTGCCCTGGCCCAGAAGCCAG 79482
Query 1408 GCGTCTACACCAAAGTCAGTGA CTCCGGGAGTGGATCTTCCAGGCCATAAAG 1460
Sbjct 79483 GCGTCTACACCAAAGTCAGTGA CTCCGGGAGTGGATCTTCCAGGCCATAAAG 79535

Score = 313 bits (169), Expect = 2e-81
Identities = 172/173 (99%), Gaps = 1/173 (0%)
Strand=Plus/Plus

Query 695 CCA-AGACTGTGGCCGAGGAAGCTGCCCGTGGACCGCATCGTGGGAGGCCGGGACACCA 753
Sbjct 73844 CCACAGACTGTGGCCGAGGAAGCTGCCCGTGGACCGCATCGTGGGAGGCCGGGACACCA 73903
Query 754 GCTTGGGCGGCTGGCCGTGGCAAGTCAGCCTTCGCTATGATGGAGCACACCTCTGTGGGG 813
Sbjct 73904 GCTTGGGCGGCTGGCCGTGGCAAGTCAGCCTTCGCTATGATGGAGCACACCTCTGTGGGG 73963
Query 814 GATCCCTGCTCTCCGGGGACTGGGTGCTGACAGCCGCCCACTGCTTCCCGGAG 866
Sbjct 73964 GATCCCTGCTCTCCGGGGACTGGGTGCTGACAGCCGCCCACTGCTTCCCGGAG 74016

Score = 289 bits (156), Expect = 4e-74
Identities = 156/156 (100%), Gaps = 0/156 (0%)
Strand=Plus/Plus

Query 38 CAGGTGAGGCAGCCTGGCCTAGCAGGCCCCACGCCACCGCCTCTGCCTCCAGGCCGCCCC 97
Sbjct 55222 CAGGTGAGGCAGCCTGGCCTAGCAGGCCCCACGCCACCGCCTCTGCCTCCAGGCCGCCCC 55281
Query 98 CTGCTGCGGGGCCACCATGCTCCTGCCAGGCTGGAGACTGACCCGACCCCGGCACTAC 157
Sbjct 55282 CTGCTGCGGGGCCACCATGCTCCTGCCAGGCTGGAGACTGACCCGACCCCGGCACTAC 55341
Query 158 CTCGAGGCTCCGCCCCACCTGCTGGACCCAGGGT 193
Sbjct 55342 CTCGAGGCTCCGCCCCACCTGCTGGACCCAGGGT 55377

Score = 268 bits (145), Expect = 5e-68
Identities = 145/145 (100%), Gaps = 0/145 (0%)
Strand=Plus/Plus

Query 1152 GGCCAAACAGGCCGGGGTACTCCAGGAGGCTCGAGTCCCCATAATCAGCAATGATGTCTGC 1211
Sbjct 79041 GGCCAAACAGGCCGGGGTACTCCAGGAGGCTCGAGTCCCCATAATCAGCAATGATGTCTGC 79100
Query 1212 AATGGCGCTGACTTCTATGGAACAGATCAAGCCCAAGATGTTCTGTGCTGGCTACCCC 1271
Sbjct 79101 AATGGCGCTGACTTCTATGGAACAGATCAAGCCCAAGATGTTCTGTGCTGGCTACCCC 79160
Query 1272 GAGGGTGGCATTGATGCCTGCCAGG 1296
Sbjct 79161 GAGGGTGGCATTGATGCCTGCCAGG 79185

Score = 248 bits (134), Expect = 6e-62
Identities = 134/134 (100%), Gaps = 0/134 (0%)
Strand=Plus/Plus

```

Query  403      CAGTGCAGGTCAGCTCTGCGGACGCTCGGCTCATGGTCTTTGACAAGACGGAAGGGACGT 462
Sbjct  73173     CAGTGCAGGTCAGCTCTGCGGACGCTCGGCTCATGGTCTTTGACAAGACGGAAGGGACGT 73232

Query  463      GGC G G C T G C T G T G C T C C T C G C G T C C A A C G C C A G G G T A G C C G G A C T C A G C T G C G A G G A G A 522
Sbjct  73233     G G C G G C T G C T G T G C T C C T C G C G T C C A A C G C C A G G G T A G C C G G A C T C A G C T G C G A G G A G A 73292

Query  523      T G G G C T T C C T C A G G      536
Sbjct  73293     T G G G C T T C C T C A G G      73306

```

Score = 233 bits (126), Expect = 2e-57
 Identities = 129/130 (99%), Gaps = 1/130 (0%)
 Strand=Plus/Plus

```

Query  533      C A G G G C A C T G A C C C A C T C C G A G C T G G A C G T G C G A A C G G C G G G C C C A A T G G C A C G T C G G G 592
Sbjct  73374     C A G G G C A C T G A C C C A C T C C G A G C T G G A C G T G C G A A C G G C G G G C C C A A T G G C A C G T C G G G 73433

Query  593      C T T C T T C T G T G T G G A C G A G G G G A G G C T G C C C C A C A C C C A G A G G C T G C T G G A G G T C A T C T C 652
Sbjct  73434     C T T C T T C T G T G T G G A C G A G G G G A G G C T G C C C C A C A C C C A G A G G C T G C T G G A G G T C A T C T C 73493

Query  653      C G T G T G - T G A      661
Sbjct  73494     C G T G T G T G A      73503

```

Score = 193 bits (104), Expect = 3e-45
 Identities = 104/104 (100%), Gaps = 0/104 (0%)
 Strand=Plus/Plus

```

Query  1050     C T C A C A G A A T A C A T C C A G C C T G T G T G C C T C C C A G C T G C C G G C C A G G C C C T G G T G G A T G G C 1109
Sbjct  78746      C T C A C A G A A T A C A T C C A G C C T G T G T G C C T C C C A G C T G C C G G C C A G G C C C T G G T G G A T G G C 78805

Query  1110     A A G A T C T G T A C C G T G A C G G G C T G G G G C A A C A C G C A G T A C T A T G G      1153
Sbjct  78806      A A G A T C T G T A C C G T G A C G G G C T G G G G C A A C A C G C A G T A C T A T G G      78849

```

Score = 191 bits (103), Expect = 1e-44
 Identities = 103/103 (100%), Gaps = 0/103 (0%)
 Strand=Plus/Plus

```

Query  261      G G T G G C C G G A C T G T G C C A T G C T G C T C C A G A C C C A A G G T G G C A G C T C T C A C T G C G G G G A C C 320
Sbjct  62792     G G T G G C C G G A C T G T G C C A T G C T G C T C C A G A C C C A A G G T G G C A G C T C T C A C T G C G G G G A C C 62851

Query  321      C T G C T A C T T C T G A C A G C C A T C G G G G C G G C A T C C T G G G C C A T T G      363
Sbjct  62852     C T G C T A C T T C T G A C A G C C A T C G G G G C G G C A T C C T G G G C C A T T G      62894

```

Score = 137 bits (74), Expect = 1e-28
 Identities = 74/74 (100%), Gaps = 0/74 (0%)
 Strand=Plus/Plus

```

Query  191      G G T C C C A C C C T G G C C C A G G A G G T C A G C C A G G G A A T C A T T A A C A A G A G G C A G T G A C A T G G C 250
Sbjct  55955     G G T C C C A C C C T G G C C C A G G A G G T C A G C C A G G G A A T C A T T A A C A A G A G G C A G T G A C A T G G C 56014

Query  251      G C A G A A G G A G G T G      264
Sbjct  56015     G C A G A A G G A G G T G      56028

```

Score = 82.4 bits (44), Expect = 7e-12
 Identities = 44/44 (100%), Gaps = 0/44 (0%)
 Strand=Plus/Plus

```

Query  1        T C G A G C C C G C T T T C C A G G G A C C C T A C C T G A G G G C C C A C A G G T G A      44
Sbjct  54009     T C G A G C C C G C T T T C C A G G G A C C C T A C C T G A G G G C C C A C A G G T G A      54052

```

Score = 80.5 bits (43), Expect = 2e-11
 Identities = 43/43 (100%), Gaps = 0/43 (0%)
 Strand=Plus/Plus

```

Query  363      G T G G C T G T T C C T C A G G A G T G A C C A G G A G C C G C T G T A C C C A G      405
Sbjct  62977     G T G G C T G T T C C T C A G G A G T G A C C A G G A G C C G C T G T A C C C A G      63019


```

Score = 78.7 bits (42), Expect = 9e-11
 Identities = 42/42 (100%), Gaps = 0/42 (0%)
 Strand=Plus/Plus

```

Query  658      G T G A T T G C C C C A G A G G C C G T T T C T T G G C C G C C A T C T G C C A A G      699
Sbjct  73631     G T G A T T G C C C C A G A G G C C G T T T C T T G G C C G C C A T C T G C C A A G      73672

```

>dbj|AK125670.1|  Homo sapiens cDNA FLJ43682 fis, clone TBAES2001258, weakly similar to SERINE PROTEASE HEPsin (EC 3.4.21.-)
Length=2831

Sort alignments for this subject sequence by:
E value Score Percent identity
Query start position Subject start position

Score = 353 bits (191), Expect = 1e-93
Identities = 199/202 (98%), Gaps = 3/202 (1%)
Strand=Plus/Plus

```
Query 858  TTCCC-GG-A-GCGGAACCGGGTCCTGTCCCGATGGCGAGTGTGTTGCCGGTGCCGTGGCC 914
Sbjct 1437  TTCCCTGGTAGGCGGAACCGGGTCCTGTCCCGATGGCGAGTGTGTTGCCGGTGCCGTGGCC 1496

Query 915  CAGGCCTCTCCCCACGGTCTGCAGCTGGGGGTGCAGGCTGTGGTCTACACGGGGGCTAT 974
Sbjct 1497  CAGGCCTCTCCCCACGGTCTGCAGCTGGGGGTGCAGGCTGTGGTCTACACGGGGGCTAT 1556

Query 975  CTTCCCTTTTCGGGACCCCAACAGCGAGGAGAACAGCAACGATATTGCCCTGGTCCACCTC 1034
Sbjct 1557  CTTCCCTTTTCGGGACCCCAACAGCGAGGAGAACAGCAACGATATTGCCCTGGTCCACCTC 1616

Query 1035  TCCAGTCCCTGCCCCCTCACAG 1056
Sbjct 1617  TCCAGTCCCTGCCCCCTCACAG 1638
```

Score = 313 bits (169), Expect = 2e-81
Identities = 172/173 (99%), Gaps = 1/173 (0%)
Strand=Plus/Plus

```
Query 695  CCA-AGACTGTGGCCGAGGAAGCTGCCCCGTGGACCGCATCGTGGGAGGCCGGGACACCA 753
Sbjct 1162  CCACAGACTGTGGCCGAGGAAGCTGCCCCGTGGACCGCATCGTGGGAGGCCGGGACACCA 1221

Query 754  GCTTGGGCCGGTGGCCGTGGCAAGTCAGCCTTCGCTATGATGGAGCACACCTCTGTGGGG 813
Sbjct 1222  GCTTGGGCCGGTGGCCGTGGCAAGTCAGCCTTCGCTATGATGGAGCACACCTCTGTGGGG 1281

Query 814  GATCCCTGCTCTCCGGGACTGGGTGCTGACAGCCGCCCACTGCTTCCCGGAG 866
Sbjct 1282  GATCCCTGCTCTCCGGGACTGGGTGCTGACAGCCGCCCACTGCTTCCCGGAG 1334
```

Score = 248 bits (134), Expect = 6e-62
Identities = 134/134 (100%), Gaps = 0/134 (0%)
Strand=Plus/Plus

```
Query 403  CAGTGCAGGTCAGCTCTGCGGACGCTCGGCTCATGGTCTTTGACAAGACGGAAGGGACGT 462
Sbjct 490  CAGTGCAGGTCAGCTCTGCGGACGCTCGGCTCATGGTCTTTGACAAGACGGAAGGGACGT 549

Query 463  GGCGGCTGTGTGCTCCTCGCGCTCCAACGCCAGGGTAGCCGGACTCAGCTGCGAGGAGA 522
Sbjct 550  GGCGGCTGTGTGCTCCTCGCGCTCCAACGCCAGGGTAGCCGGACTCAGCTGCGAGGAGA 609

Query 523  TGGGCTTCCTCAGG 536
Sbjct 610  TGGGCTTCCTCAGG 623
```

Score = 233 bits (126), Expect = 2e-57
Identities = 129/130 (99%), Gaps = 1/130 (0%)
Strand=Plus/Plus


```
Query 533  CAGGGCACTGACCCACTCCGAGCTGGACGTGCGAACGGCGGGCGCCAATGGCACGTCGGG 592
Sbjct 691  CAGGGCACTGACCCACTCCGAGCTGGACGTGCGAACGGCGGGCGCCAATGGCACGTCGGG 750

Query 593  CTTCTTCTGTGTGGACGAGGGGAGGCTGCCCCACACCCAGAGGCTGCTGGAGGTCATCTC 652
Sbjct 751  CTTCTTCTGTGTGGACGAGGGGAGGCTGCCCCACACCCAGAGGCTGCTGGAGGTCATCTC 810

Query 653  CGTGTG-TGA 661
Sbjct 811  CGTGTGGTGA 820
```

Score = 78.7 bits (42), Expect = 9e-11
Identities = 42/42 (100%), Gaps = 0/42 (0%)
Strand=Plus/Plus

```
Query 658  GTGATTGCCCCAGAGGCCGTTTCTTGCCGCCATCTGCCAAG 699
Sbjct 948  GTGATTGCCCCAGAGGCCGTTTCTTGCCGCCATCTGCCAAG 989
```

>gb|DQ677665.1|  Homo sapiens sodium channel beta-1 subunit precursor (SCN1B)
gene, complete cds
Length=15819

Sort alignments for this subject sequence by:
E value Score Percent identity
Query start position Subject start position

Score = 289 bits (156), Expect = 4e-74
 Identities = 156/156 (100%), Gaps = 0/156 (0%)
 Strand=Plus/Plus

```

Query 38      CAGGTGAGGCAGCCTGGCCTAGCAGGCCCCACGCCACCGCCTCTGCCTCCAGGCCGCCCG 97
Sbjct 14090   CAGGTGAGGCAGCCTGGCCTAGCAGGCCCCACGCCACCGCCTCTGCCTCCAGGCCGCCCG 14149

Query 98      CTGCTGCGGGGCCACCATGCTCCTGCCCAGGCCTGGAGACTGACCCGACCCCGGCACTAC 157
Sbjct 14150   CTGCTGCGGGGCCACCATGCTCCTGCCCAGGCCTGGAGACTGACCCGACCCCGGCACTAC 14209

Query 158     CTCGAGGCTCCGCCCCACCTGCTGGACCCAGGGT 193
Sbjct 14210   CTCGAGGCTCCGCCCCACCTGCTGGACCCAGGGT 14245

```

Score = 137 bits (74), Expect = 1e-28
 Identities = 74/74 (100%), Gaps = 0/74 (0%)
 Strand=Plus/Plus

```

Query 191     GGTCCACCCCTGGCCCAGGAGGTAGCCAGGGAATCATTAAACAAGAGGCAGTGACATGGC 250
Sbjct 14823   GGTCCACCCCTGGCCCAGGAGGTAGCCAGGGAATCATTAAACAAGAGGCAGTGACATGGC 14882

Query 251     GCAGAAGGAGGGTG 264
Sbjct 14883   GCAGAAGGAGGGTG 14896


```

Score = 82.4 bits (44), Expect = 7e-12
 Identities = 44/44 (100%), Gaps = 0/44 (0%)
 Strand=Plus/Plus

```

Query 1       TCGAGCCCGCTTTCCAGGGACCTACCTGAGGGCCACAGGTGA 44
Sbjct 12877   TCGAGCCCGCTTTCCAGGGACCTACCTGAGGGCCACAGGTGA 12920

```

>gb|AC197610.3|  MACACA MULATTA BAC clone CH250-348G8 from chromosome 19, complete sequence
 Length=158733

Sort alignments for this subject sequence by:
 E value Score Percent identity
 Query start position Subject start position

Score = 250 bits (135), Expect = 2e-62
 Identities = 149/156 (95%), Gaps = 0/156 (0%)
 Strand=Plus/Plus

```

Query 38      CAGGTGAGGCAGCCTGGCCTAGCAGGCCCCACGCCACCGCCTCTGCCTCCAGGCCGCCCG 97
Sbjct 149463   CAGGTGAGGCAGCCTGGCCTAGCAGGCCCCACGCCACCGCCTCTGCCTCCAGGCCACCCG 149522

Query 98      CTGCTGCGGGGCCACCATGCTCCTGCCCAGGCCTGGAGACTGACCCGACCCCGGCACTAC 157
Sbjct 149523   CTGCTGCGGGGCCACCATGCTCCTGCCCAGGCCTGGAGACTGACCCGACCCCGGAACCAC 149582

Query 158     CTCGAGGCTCCGCCCCACCTGCTGGACCCAGGGT 193
Sbjct 149583   CTCGAGGCTCCGCCCCACCTGCTGGACCCAGGGT 149618

```

Score = 180 bits (97), Expect = 2e-41
 Identities = 101/103 (98%), Gaps = 0/103 (0%)
 Strand=Plus/Plus

```

Query 261     GGTGGCCGGACTGTGCCATGCTGTCTCCAGACCCAAGGTGGCAGCTCTCACTGCGGGGACC 320
Sbjct 157187   GGTGGCCGGACTGTGCCATGCTGTCTCCAGACCCAAGGTGGCAGCTCTCACTGCGGGGACC 157246

Query 321     CTGCTACTTCTGACAGCCATCGGGGCGGCATCCTGGGCCATTG 363
Sbjct 157247   CTGCTACTTCTGACAGCCATCGGGGCGGCATCCTGGGCCATTG 157289

```

Score = 132 bits (71), Expect = 6e-27
 Identities = 73/74 (98%), Gaps = 0/74 (0%)
 Strand=Plus/Plus

```

Query 191     GGTCCACCCCTGGCCCAGGAGGTAGCCAGGGAATCATTAAACAAGAGGCAGTGACATGGC 250
Sbjct 150194   GGTCCACCCCTGGCCCAGGAGGTAGCCAGGGAATCATTAAACAAGAGGCAGTGACATGGC 150253

Query 251     GCAGAAGGAGGGTG 264
Sbjct 150254   GCAGAAGGAGGGTG 150267


```

Score = 75.0 bits (40), Expect = 1e-09
 Identities = 42/43 (97%), Gaps = 0/43 (0%)
 Strand=Plus/Plus

```

Query 363     GTGGCTGTTCTCCTCAGGAGTGACCAGGAGCCGCTGTACCCAG 405
Sbjct 157372   GTGGCTGTTCTCCTCAGGAGTGACCAGGAGCCGCTGTACCCAG 157414


```

>ref|XM_001719305.1|  PREDICTED: Homo sapiens hypothetical protein LOC100128675 (LOC100128675), mRNA
Length=1287

Score = 207 bits (112), Expect = 1e-49
Identities = 112/112 (100%), Gaps = 0/112 (0%)
Strand=Plus/Minus

```
Query  403  CAGTGCAGGTCAGCTCTGCGGACGCTCGGCTCATGGTCTTTGACAAGACGGAAGGGACGT  462
          |||||
Sbjct  513  CAGTGCAGGTCAGCTCTGCGGACGCTCGGCTCATGGTCTTTGACAAGACGGAAGGGACGT  454


Query  463  GCGCGCTGCTGTGCTCCTCGCGCTCCAACGCCAGGGTAGCCGGACTCAGCTG  514
          |||||
Sbjct  453  GCGCGCTGCTGTGCTCCTCGCGCTCCAACGCCAGGGTAGCCGGACTCAGCTG  402
```

>ref|XM_001721961.1|  PREDICTED: Homo sapiens hypothetical protein LOC100128675 (LOC100128675), mRNA
Length=1287

Score = 207 bits (112), Expect = 1e-49
Identities = 112/112 (100%), Gaps = 0/112 (0%)
Strand=Plus/Minus

```
Query  403  CAGTGCAGGTCAGCTCTGCGGACGCTCGGCTCATGGTCTTTGACAAGACGGAAGGGACGT  462
          |||||
Sbjct  513  CAGTGCAGGTCAGCTCTGCGGACGCTCGGCTCATGGTCTTTGACAAGACGGAAGGGACGT  454


Query  463  GCGCGCTGCTGTGCTCCTCGCGCTCCAACGCCAGGGTAGCCGGACTCAGCTG  514
          |||||
Sbjct  453  GCGCGCTGCTGTGCTCCTCGCGCTCCAACGCCAGGGTAGCCGGACTCAGCTG  402
```

>ref|XM_001719287.1|  PREDICTED: Homo sapiens hypothetical protein LOC100128675 (LOC100128675), mRNA
Length=1287

Score = 207 bits (112), Expect = 1e-49
Identities = 112/112 (100%), Gaps = 0/112 (0%)
Strand=Plus/Minus

```
Query  403  CAGTGCAGGTCAGCTCTGCGGACGCTCGGCTCATGGTCTTTGACAAGACGGAAGGGACGT  462
          |||||
Sbjct  513  CAGTGCAGGTCAGCTCTGCGGACGCTCGGCTCATGGTCTTTGACAAGACGGAAGGGACGT  454

Query  463  GCGCGCTGCTGTGCTCCTCGCGCTCCAACGCCAGGGTAGCCGGACTCAGCTG  514
          |||||
Sbjct  453  GCGCGCTGCTGTGCTCCTCGCGCTCCAACGCCAGGGTAGCCGGACTCAGCTG  402
```

>gb|AC158993.2|  Mus musculus BAC clone RP24-427N13 from chromosome 7, complete sequence
Length=179746

Sort alignments for this subject sequence by:
E value Score Percent identity
Query start position Subject start position

Score = 141 bits (76), Expect = 1e-29
Identities = 122/145 (84%), Gaps = 0/145 (0%)
Strand=Plus/Minus

```
Query  1152  GGCCAACAGGCGGGTACTCCAGGAGGCTCGAGTCCCCATAATCAGCAATGATGTCTGC  1211
          |||||
Sbjct  61803  GGCCAACAGGCTATGGTGCTCCAAGAGGCCCGGGTCCCATCATAAGCAACGAAGTTGC  61744

Query  1212  AATGGCGCTGACTTCTATGGAAACAGATCAAGCCCAAGATGTTCTGTGCTGGCTACCCC  1271
          |||||
Sbjct  61743  AACAGCCCCGACTTCTACGGGAATCAGATCAAGCCCAAGATGTTCTGTGCTGGCTATCCT  61684

Query  1272  GAGGGTGGCATTGATGCCTGCCAGG  1296
          |||||
Sbjct  61683  GAGGGTGGCATTGATGCGTGCCAGG  61659
```

Score = 119 bits (64), Expect = 5e-23
Identities = 92/105 (87%), Gaps = 4/105 (3%)
Strand=Plus/Minus

```
Query  261  GGTGGCCGGACTG-TGCCATGCTGTCCAGACCCAAGGTGGCAGCTCTCACTGCGGGGAC  319
          |||||
Sbjct  71347  GGTGGCCGGACTGCAG-CATGCTGTCTCCAGACCCAAGGTGGCAGCTCTCATGTGGGTAC  71289

Query  320  CCTGCTACTTC-TGACAGCCATCGGGGCGGCATCCTGGGCCATTG  363
          |||||
Sbjct  71288  CCTGCTG-TTCCTGACAGGCATTGGGGCGCGTCTCTGGGCCATTG  71245
```

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)

Posted date: May 19, 2008 5:44 PM

Number of letters in database: -2,000,849,822

Number of sequences in database: 6,839,787

Lambda	K	H
1.33	0.621	1.12

Gapped

Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2

Gap Penalties: Existence: 0, Extension: 0

Number of Sequences: 6839787

Number of Hits to DB: 3671278

Number of extensions: 17

Number of successful extensions: 17

Number of sequences better than 10: 3

Number of HSP's better than 10 without gapping: 0

Number of HSP's gapped: 16

Number of HSP's successfully gapped: 16

Length of query: 1783

Length of database: 23768953950

Length adjustment: 33

Effective length of query: 1750

Effective length of database: 23543240979

Effective search space: 41200671713250

Effective search space used: 41200671713250

A: 0

X1: 15 (28.8 bits)

X2: 32 (59.1 bits)

X3: 54 (99.7 bits)

S1: 15 (28.8 bits)

S2: 23 (43.6 bits)